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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 12:32:55 : Search time 3720.62 Seconds  
(without alignments)  
11745.631 Million cell updates/sec

Title: US-09-486-757-10  
Perfect score: 2649  
Sequence: 1 cggcagagctttagtat.....ttttgagaaaaa 2649

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1472140 seqs, 8248589755 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_em.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_om.\*
- 20: em\_or.\*
- 21: em\_ov.\*
- 22: em\_pat.\*
- 23: em\_ph.\*
- 24: em\_pl.\*
- 25: em\_ro.\*
- 26: em\_sts.\*
- 27: em\_sy.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htgo\_hum.\*
- 31: em\_htgo\_inv.\*
- 32: em\_htgo\_rod.\*
- 33: em\_htg\_hum.\*
- 34: em\_htg\_inv.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2547	96.1	2650	8	PSU67185	U67185 Papaver som
2	29	1.1	2493	8	AF302497	AF302497 Hybrid po
3	26	1.0	2114	6	A75959	A75959 Sequence 1
4	26	1.0	2199	8	ATATRIG	X66016 A.thaliana
5	26	1.0	2498	8	AF302496	AF302496 Hybrid po
6	26	1.0	125803	8	ATF22K18	AL035356 Arabidops
7	26	1.0	198402	8	ATCHRIV61	AL161561 Arabidops
8	24	0.9	2641	8	VSNER	Z26252 V.sativa mr
9	24	0.9	129332	9	AL590028	AL590028 Human DNA
10	24	0.9	161486	2	AL590008	AL590008 Homo sapi
11	24	0.9	163603	2	AC026755	AC026755 Homo sapi
12	23	0.9	1864	10	BC011090	BC011090 Mus muscu
13	23	0.9	2466	8	AF024634	AF024634 Petroseli
14	23	0.9	2545	8	AF002698	AF002698 Pisum sat
15	23	0.9	2617	8	VIRNADPH4	L07843 Vigna radi
16	23	0.9	2631	8	PM14CPR	Z49767 Pseudotsuga
17	23	0.9	160708	2	AC068406	AC068406 Homo sapi
18	22	0.8	1821	8	AB007405	AB007405 Oryza sat
19	22	0.8	2385	8	AF130425	AF130425 Lycopersi
20	22	0.8	2556	8	AF024635	AF024635 Petroseli
21	22	0.8	17643	8	AC079287	AC079287 Arabidops
22	22	0.8	65262	2	AC025908	AC025908 Arabidops
23	22	0.8	75133	8	F2H15	AC034106 Sequence
24	22	0.8	77040	8	AC004484	AC004484 Arabidops
25	22	0.8	87967	8	AC005223	AC005223 Arabidops
26	22	0.8	199421	2	AC051636	AC051636 Homo sapi
27	21	0.8	235	5	MGU79352	U79352 Meleagris g
28	21	0.8	266	5	AF019725	AF019725 Meleagris
29	21	0.8	425	3	PFU72623	U72623 Plasmodium
30	21	0.8	425	3	PFU72624	U72624 Plasmodium
31	21	0.8	425	3	PFU72625	U72625 Plasmodium
32	21	0.8	514	11	G22860	G22860 human STS W
33	21	0.8	1328	9	BC008615	BC008615 Homo sapi
34	21	0.8	1811	10	AF195533	AF195533 Mus muscu
35	21	0.8	1842	3	PFU27393	U27393 Plasmodium
36	21	0.8	1848	3	PFU27384	U27384 Plasmodium
37	21	0.8	1848	3	PFU27385	U27385 Plasmodium
38	21	0.8	1848	3	PFU27386	U27386 Plasmodium
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44	21	0.8	1848	3	PFU27394	U27394 Plasmodium
45	21	0.8	1848	3	PFU27395	U27395 Plasmodium

ALIGNMENTS

RESULT 1

PSU67185

LOCUS

DEFINITION

complete cds.

ACCESSION

U67185

VERSION

U67185.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

PSU67185 2650 bp mRNA 06-MAR-1998  
Papaver somniferum NADPH:ferrihemoprotein oxidoreductase mRNA,  
complete cds.  
U67185  
U67185.1 GI:2580496  
opium poppy.  
Papaver somniferum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;  
Papaveraceae; Papaver.  
1 (bases 1 to 2650)  
Rosco, A., Pauli, H.H., Priesner, W. and Kutchan, T.M.  
Cloning and heterologous expression of NADPH-cytochrome P450  
reductases from the Papaveraceae  
Arch. Biochem. Biophys. 348 (2), 369-377 (1997)  
98096363  
2 (bases 1 to 2650)



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Qy 2641 aaaaaaaaaa 2649  
Db 2641 AAAAAAAAAA 2649

RESULT 2

AF302497 LOCUS 2493 bp mRNA PLN 02-MAR-2001  
DEFINITION Hybrid poplar (Populus trichocarpa x P. deltoides) NADPH-cytochrome  
P450 oxydoreductase isoform 2 mRNA, complete cds.  
AF302497  
AF302497.1 GI:13183563

ORGANISM

Populus x generosa.  
Populus x generosa  
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
Malpighiales; Salicaceae; Populus.  
1 (bases 1 to 2493)  
Ro.D.-K. and Douglas,C.

AUTHORS

Functional characterization of cytochrome P450 reductase from the  
hybrid poplar (Populus trichocarpa x P. deltoides)  
Unpublished  
2 (bases 1 to 2493)  
Ro.D.-K. and Douglas,C.  
Direct Submission

TITLE

Submitted (05-SEP-2000) Botany, University of British Columbia,  
6270 University Blvd., Vancouver, British Columbia V6T 1Z4, Canada

JOURNAL

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

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27. .2165  
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BASE COUNT

ORIGIN

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Best Local Similarity 100.0%; Pred. No..0.00036;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

Db

385

actggtactgctgaaggatttgcctaaagc 413

360

ACTGGTACTGCTGAAGGATTTGCTAAGGC 388

RESULT 3

AF75959

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

A75959 2114 bp DNA PAT 19-OCT-1999  
Sequence 1 from Patent WO9321326.  
A75959  
A75959.1 GI:6088149  
thale cress.  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```
REFERENCE 1 (bases 1 to 2114)
AUTHORS Kazmaier, M. and Lacroite, F.
TITLE METHOD OF CLONING A DNA SEQUENCE CODING FOR A PLANT
JOURNAL NADPH-CYTOCHROME P450 REDUCTASE AND ASSOCIATED DNA SEQUENCES
PATENT: WO 9321326-A 1 28-OCT-1993;
ORSAN (FR); KAZMAIER MICHAEL (FR)
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcaacataagatgatgagaa 1979
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Db 1893 TATGTTCAACATAAGATGATGAGAA 1918

RESULT 4
LOCUS ATATRIG 2199 bp mRNA PLN 01-JUN-1992
DEFINITION A.thaliana ATRI mRNA for NADPH-cytochrome P450 reductase.
ACCESSION X66016
VERSION x66016.1 GI:16186
KEYWORDS ATRI gene; NADPH-ferrihemoprotein reductase.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 2199)
Pompon, D.M.
Direct Submission
Submitted (11-MAY-1992) D.M. Pompon, Centre de Genetique Mol du
CNRS, Avenue de la Terrasse, 91198 Gif-Sur-Yvette Cedex, FRANCE
2 (bases 1 to 2199)
Mignote-Vieux, C., Kazmaier, M., Lacroite, F. and Pompon, D.M.
Unpublished
Location/Qualifiers
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REFERENCE 1 (bases 1 to 2114)
AUTHORS Kazmaier, M. and Lacroite, F.
TITLE METHOD OF CLONING A DNA SEQUENCE CODING FOR A PLANT
JOURNAL NADPH-CYTOCHROME P450 REDUCTASE AND ASSOCIATED DNA SEQUENCES
PATENT: WO 9321326-A 1 28-OCT-1993;
ORSAN (FR); KAZMAIER MICHAEL (FR)
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BASE COUNT 603 a 399 c 542 g 570 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcaacataagatgatgagaa 1979
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Db 1927 TATGTTCAACATAAGATGATGAGAA 1952

RESULT 5
LOCUS AF302496 2498 bp mRNA PLN 02-MAR-2001
DEFINITION Hybrid poplar (Populus trichocarpa x P. deltoides) NADPH-cytochrome
P450 oxydoreductase isoform 1 mRNA, complete cds.
ACCESSION AF302496
VERSION AF302496.1 GI:13183561
KEYWORDS
SOURCE
ORGANISM Populus x generosa.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Malpighiales; Salicaceae; Populus.
1 (bases 1 to 2498)
Ro, D.-K. and Douglas, C.
Functional characterization of cytochrome P450 reductase from the
hybrid poplar (Populus trichocarpa X P. deltoides)
Unpublished
2 (bases 1 to 2498)
Ro, D.-K. and Douglas, C.
Direct Submission
Submitted (05-SEP-2000) Botany, University of British Columbia,
6270 University Blvd., Vancouver, British Columbia V6T 1Z4, Canada
Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1946 aagaagaatatttcaacataagatg 1971
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Db 1933 AGAAGGAATATGTCACATAAGATG 1958

RESULT 6
ATF22K18 125803 bp DNA PLN 03-FEB-1999
LOCUS
DEFINITION Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII
project).
ACCESSION AL035356
VERSION AL035356.1 GI:4220510
KEYWORDS
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 125803)
Bevan, M., Wedler, H., Wedler, E., Wambutt, R., Hoheisel, J.,
Mewes, H.W., Mayer, K.F.X. and Schueller, C.
Unpublished
EU Arabidopsis sequencing, project.
2 (bases 1 to 125803)
Direct Submission
Submitted (03-FEB-1999) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
schueller@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbc.ac.uk
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosome 4 can be
viewed at: http://websvr.mips.biochem.mpg.de/proj/thal/.
FEATURES
source
1. 125803
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/db_xref="taxon:3702"
/chromosome="4"
171..2980
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complement(join(171..601,689..883,983..1159,1250..1469,
1556..2980))
/gene="F22K18.10"
complement(171..601)
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CDS
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/note="similarity to DNA polymerase III gamma subunit -
Aquifex aeolicus, F1R2:A70460
Contains ATP/GTP-binding site motif A (P-loop) [GPRGTGKT]"
/codon_start=1
/product="DNA polymerase III like protein"
/protein_id="CAA22984.1"
/db_xref="GI:4220511"
/translation="MGETRRHSVDVPTITLVALRRVRSURDPCTTSMKFSALLDNV
KWTGNGNGISIQFVHADDAKCAADAPVGLIPFGSYSIMEELEGCDLHKLSKVI
NVBGDASRSRSCSDLSVKGRDLACNAPSIHVEAGSGGRYRTHYSFKLASSVGE
YSGRLGSPNNTNHSYVGDEVDVFDQSNGRCGITYCWSPTPRYRGSNOSSDVEEYPL
LPNGSGEDSVYTPSHVLSRLSQFRPKSFDLVCQEVVVKCLLSTILGRITSVY
LFHGPGRGTSTSKFAAALNCLSQAAHSRPGCLCECKSYFSGRGRDWMETDYGKL
NPSYLSRSLTKSASLPVSSRFKFIIDECQLLCOETGWTLLNSLDFNSQHSVFILVT
RSEYLAKEKSKMLIADFSQVLGCNVEIQMLNLIISACSPKSAKAAASLFFGLFSCS
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/number=4
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3345..3371
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8981..9090
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8981..10571
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join(8981..9090,9370..10119,10217..10571)
/gene="F22K18.20"
/note="strong similarity to pectate lyase, Musa acuminata,
PATX:E209876"
/codon_start=1
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/protein_id="CAA22985.1"
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GRKGLYLSCTTCNPIDDCWCRDPHWOHQRLADCAICGKNAICGRDGRIVYVTDG
GNDNPVSPKPTLURHAVQDEPLIIFORDMTIQLKEELIWNFKTIDGRGASVHISG
GPCITIOYVTNIIIGHIHIDCKQGNAMVSRPHFGWRTISDGDGVSIFGGSHVWV
DHCFSNCEGLDIAMGSTAITLSNNHTIHDKVMLLGHSDTYSRDKNNQVTFIAFNH
FGGLVQRMPRHGYFHVWNNDYTHWEMYAIGGSANPTINSQGNRFLAPNTRFSKEVTK
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9091..9369
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/number=1
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/number=2
10120..10216
/gene="F22K18.20"

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 /gene="F22K18.30"  
 /note="cp31 is 100% homologous but lacks a 15 AS stretch  
 in the first exon, position 106 to 120  
 Ribonucleoprotein  
 Contains Eukaryotic putative RNA-binding region RNP-1  
 signature [RGFGFTM], [RGFGFTM]  
 contains EST gb:AA395600, A1100105, T45260, T76407,  
 T43174, R90420, T22781, H76412, R64751, T21054, T20937,  
 N96937, AA713138"  
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 /db\_xref="GI:4220513"  
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 VNSQALMLFEQAGTVEIAEVYINRETQSGFGFTVMSVDEATAVEKFNVDLNG  
 RLITVKAAPRGSRPERAPRVYPAFRVYVGNLFDVNDGRLEQLFSEHGKVVVEARVY  
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 14535. .14816  
 /gene="F22K18.30"  
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 14817. .14913  
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 /number=3  
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 17638. .19720  
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 19247. .19720)  
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 PRRLASLHSPILSLGRLVMPVKRTYFLDIYKNIDKITLVRCPVLVHGTFADVDVDF  
 HGKQLNELCOEYPLWLGKGNHCDLELFPYIYGLKKFVSAVEKSAKRNKSNFSRRS  
 MECCEQPPHSDAPKSKDKREKPKRSIDRLRFQYKLSHIEKPKLKVPFEMERS  
 RRSVDIYRDKSQPWERARKSVVDLDRSRATE"  
 17940. .18590  
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 /number=1

exon 18591. .18627  
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 /number=2  
 18628. .18727  
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 18728. .18964  
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 QY 1954 tatgttcaacataagatgatggagaa 1979  
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 Db 117747 TATGTTCAACATAAGATGATGGAGAA 117772  
 RESULT 7  
 ATCHRIV61/c  
 LOCUS ATCHRIV61 198402 bp DNA PLN 16-MAR-2000  
 DEFINITION Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61.  
 ACCESSION AL161561  
 VERSION AL161561.2 GI:7269265  
 KEYWORDS  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 REFERENCE 1 (bases 4709 to 5139)  
 AUTHORS Robben,J., Grynoprez,B., Volckaert,G, Mewes,H.W., Lemcke,K. and  
 Mayer,K.F.X.  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 16658 to 125116)  
 AUTHORS Zimmermann,W., Grueneisen,A., Wambutt,R., Kalicki,J., Wohldmann,P.,  
 Smith,A., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.  
 JOURNAL Unpublished  
 REFERENCE 3 (bases 123107 to 198402)  
 AUTHORS Wedler,H., Wedler,E., Wambutt,R., Mewes,H.W., Lemcke,K. and  
 Mayer,K.F.X.  
 JOURNAL Unpublished  
 REFERENCE 4 (bases 1 to 20862)  
 AUTHORS Peters,S.A., van Staveren,M., Dirkse,W., Stiekema,W., Mewes,H.W.,  
 Lemcke,K. and Mayer,K.F.X.  
 JOURNAL Unpublished  
 REFERENCE 5 (bases 1 to 198402)  
 AUTHORS EU Arabidopsis sequencing,project.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer  
 Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:  
 lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project  
 Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge  
 Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,  
 E-mail: michael.bevan@bbsrc.ac.uk  
 COMMENT Information on performance of analysis and a more detailed  
 annotation of this entry and other sequences of chromosomes 3, 4  
 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/  
 this fragment has an overlap with ATCHRIV60 at the 5' end and an  
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 1. .198402  
 /organism="Arabidopsis thaliana"  
 /variety="Columbia"  
 /db\_xref="taxon:3702"  
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 7612. .9918  
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 exon  
 intron



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Query Match
Best Local Similarity 100.0%; Score 26; DB 8; Length 198402;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcacataagatgatgagaa 1979
|||||
Db 131163 TATGTTCAACATAAGATGATGAGAA 131138

/number=7
12214..12304
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LOCUS VSNER 2641 bp mRNA PLN 14-SEP-1993
DEFINITION V.sativa mRNA for NADPH-ferrihemoprotein reductase.
ACCESSION Z26252
VERSION Z26252.1 GI:400531
KEYWORDS NADPH-ferrihemoprotein reductase.
SOURCE spring vetch.
ORGANISM Vicia sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Vicia.
REFERENCE
AUTHORS Benveniste,I., Begue-Kirn,C., Lesot,A., Hasenfratz,M. and Durst,F.
TITLE Isolation and characterization of a cDNA encoding an
NADPH-cytochrome P450 reductase from Vicia sativa
JOURNAL Unpublished
AUTHORS Durst,F.
TITLE Direct Submission
SUBMITTED (13-SEP-1993) Durst F., CNRS - Institut de Biologie
Moléculaire des Plantes, Cellular and Molecular Enzymology, 28, rue
Goethe, Strasbourg, France, F-67083
FEATURES
Source
1. 2641
/organism="Vicia sativa"
/strain="Var. lolita"
/db_xref="taxon:3908"
/tissue="9a13c"
/clone_lib="lambda Zap library of I. Benveniste"
/dev_stage="7 day dark-grown seedlings"
204..2282
/EC_number="1.6.2.4"
/function="Catalyzes the reduction of cytochrome P450 in
microsomes"
/citation="[1]"
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WFTGKEERGTLQQLTYGVFALGNQYEHFNKIVDEDLTEQGAARLPVPVLGDD
QSTEDDFNAWKETLWPELDQLLDEDDVNTASTPYTAAISEYRVVTHDPTVSPSYEN
HFNVANGAVFDIHPGCRVNVAVRELHKPQSDRSCIHLEFDLSGTGTVTETGDHGV
YAENCNDTVEAGKLLGQSLDLLFLSHTDKEDGTSLGSLLLPPPGCTVTRTALACVA
DLNPPKKAIVALAHAASEPSEARLKFLLSSPGQKDEYSKWVGSORSLLLEWADFP
SAKPLPLGVAATAPRQPIYSISSPAPQPRQHVHTCALVEGPTPTGRHKGVCST
WMSKATPLEKSHDCSRAPIFRPSNFKLPADHSIPIIMVPGTGLAFPGFLQERLAL
KEDGVQLGALLFPFCRNQMDFTYEDLNNVQQGAISELIVAFSREGPEKVVQHK
MMDKAEYLWLSLISGGGLYVCGDAKGARDVHRSLSHTIVQQQENADSSKAEATVKLIQ
MDGRYLRLDVW"
713 a 511 c 615 g 802 t

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 24; DB 9; Length 129332;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 tggctactcagactggtactgctga 398
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Db 464 TGGTACTCAGACTGGTACTGCTGA 487

RESULT 9
AL590028 129332 bp DNA PRI 09-MAY-2001
LOCUS Human DNA sequence from clone RP11-384M8 on chromosome 13, complete
sequence.
ACCESSION AL590028
VERSION AL590028.7 GI:14018310
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Peck,A.
TITLE Direct Submission
JOURNAL Submitted (09-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT
On May 11, 2001 this sequence version replaced gi:13990191.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em., EMBL; Sw.,
SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C-elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chrl3
RP11-384M8 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-384M8. It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP11-131P10 is at 129233 in this
sequence. The true right end of clone RP11-19612 is at 100 in this
sequence.
FEATURES
Source
1. 129332
/organism="Homo sapiens"
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/chromosome="13"
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/clone_id="23685 c 23101 g 37543 t"
BASE COUNT 45003 a 23685 c 23101 g 37543 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 24; DB 9; Length 129332;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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misc_feature 1. .1835
/note="assembly_name:Contig27"
misc_feature 1936. .21856
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misc_feature 21757. .163603
/note="assembly_name:Contig34
clone_end:SP6"
BASE COUNT 56206 a 29637 c 28754 g 48804 t 202 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2626 agagttttgagaaaaa 2649
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Db 43242 AGAGTTTGGAGAAAAA 43265

RESULT 12
BC011090 1864 bp mRNA ROD 30-JUL-2001
LOCUS Mus musculus, Similar to DnaJ (Hsp40) homolog, subfamily B, member
DEFINITION 10. clone MGC:19256 IMAGE:3968468, mRNA, complete cds.
ACCESSION BC011090
VERSION BC011090.1 GI:15029742
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1864)
Strausberg,R.
Direct Submission
Submitted (25-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalobebcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 23 Row: j Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, GenomeScan gene prediction, Similarity but not identity
to protein.

FEATURES
source 1. .1864
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model. 10 month old virgin mouse. Taken by biopsy."
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/lab_host="DH10B"
/note="vector: pcmw-SPORT6"
102. .935
CDS

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SRREQPSVAPGLGVQVRPTSLSRPPDHLSEDEDLQALAMAYSLSEMAAGQPADV
F"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2627 gagtttgagaaaaa 2649
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Db 1812 GAGTTTGGAGAAAAA 1834

RESULT 13
AF024634 2466 bp mRNA PLN 26-JAN-1998
LOCUS Petroselinum crispum NADPH cytochrome P450 reductase (CPR2) mRNA,
DEFINITION complete cds.
ACCESSION AF024634
VERSION AF024634.1 GI:2809384
KEYWORDS parsley.
SOURCE Petroselinum crispum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
1 (bases 1 to 2466)
Koopmann,E. and Hahlbrock,K.
Differentially regulated NADPH:cytochrome P450 oxidoreductases in
parsley
Proc. Natl. Acad. Sci. U.S.A. 94 (26), 14954-14959 (1997)
98070859
REFERENCE 2 (bases 1 to 2466)
Koopmann,E. and Hahlbrock,K.
Direct Submission
TITLE Parsley
JOURNAL Submitted (12-SEP-1997) Biochemistry, Max-Planck-Institut fuer
Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln 50829, Germany
Location/Qualifiers
1. .2466
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/db_xref="taxon:4043"
1. .2466
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76. .2121
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/note="oxidoreductase"
/codon_start=1
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/protein_id="AAB97736.1"
/db_xref="GI:2809385"
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AKFRVDDDDYAAEDEYEAKFKESFAFFFLATYGDGPTDNNARYFNKFSSEEGK
DWLNKLOYGVGFGNROYEHFNKIAKVDDGLADQAKRIVEGMGDDQCIDDDFTA
WRRLWPELDKLLDDEDTSAATPYAAVLEYRVVYDQDLDATLDRSLTQNGHTVH
DAQPCRSSVAARKKELHKPADRSCHLEFDISHTGLAYETGHDVGYCNLVIVE
AEKLLGMQNPYFVSHIDDEGTPLTGSLPPPPCTVRSALAKYADLLSSPKKSL
LALAAHASDPTADRLRLASAPKAGDEYAQWVVAHSLELVLAEPFSAKPLGVFA
SVAPRLQPRYISSSSPRWPSRIHVTCALVYKTPGRIGHKGCSTWMMKNVLSLE
HDCSWAPFVFRQSNFKLPSTKVPITIMIGPTGLAPRGTQLQRQALQKADGAELGTAV
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CDS



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3'UTR          GRYLRDWM
2245. .2617
polyA_site     2617
BASE COUNT     668 a 512 c 622 g 815 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 463 gttgacctggtgactatgcagc 485
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Db 520 GTTGACCTGGATGACTATGCAGC 542

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Search completed: December 27, 2001, 16:27:54  
Job time: 14099 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 14:12:15 ; Search time 222.02 Seconds  
(without alignments)  
10229.054 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649

Sequence: 1 cggcagcgactgttagtat.....tttgagaaaaaaaaaaaaa 2649

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_1101:\*

1:	/SIDS2/gcgdata/geneseq/geneseq/NA1980.DAT:*
2:	/SIDS2/gcgdata/geneseq/geneseq/NA1981.DAT:*
3:	/SIDS2/gcgdata/geneseq/geneseq/NA1982.DAT:*
4:	/SIDS2/gcgdata/geneseq/geneseq/NA1983.DAT:*
5:	/SIDS2/gcgdata/geneseq/geneseq/NA1984.DAT:*
6:	/SIDS2/gcgdata/geneseq/geneseq/NA1985.DAT:*
7:	/SIDS2/gcgdata/geneseq/geneseq/NA1986.DAT:*
8:	/SIDS2/gcgdata/geneseq/geneseq/NA1987.DAT:*
9:	/SIDS2/gcgdata/geneseq/geneseq/NA1988.DAT:*
10:	/SIDS2/gcgdata/geneseq/geneseq/NA1989.DAT:*
11:	/SIDS2/gcgdata/geneseq/geneseq/NA1990.DAT:*
12:	/SIDS2/gcgdata/geneseq/geneseq/NA1991.DAT:*
13:	/SIDS2/gcgdata/geneseq/geneseq/NA1992.DAT:*
14:	/SIDS2/gcgdata/geneseq/geneseq/NA1993.DAT:*
15:	/SIDS2/gcgdata/geneseq/geneseq/NA1994.DAT:*
16:	/SIDS2/gcgdata/geneseq/geneseq/NA1995.DAT:*
17:	/SIDS2/gcgdata/geneseq/geneseq/NA1996.DAT:*
18:	/SIDS2/gcgdata/geneseq/geneseq/NA1997.DAT:*
19:	/SIDS2/gcgdata/geneseq/geneseq/NA1998.DAT:*
20:	/SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT:*
21:	/SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT:*
22:	/SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2547	96.1	2650	20 AAX08517	Poppy cytochrome p
2	26	1.0	2114	14 AAO51236	Plant NADPH cytoch
3	22	0.8	600	21 AAC98382	Human colon cancer
4	21	0.8	4507	16 AAO83525	SABP gene. Plasm
5	21	0.8	4507	18 AAO72888	Sialic acid bindin
6	21	0.8	4507	21 AA298282	P. falciparum SABB
7	20	0.8	306	21 AAC74719	Human ORFX ORF274
8	20	0.8	485	21 AAC35800	Zea mays DNA fragm
9	20	0.8	531	21 AAA46546	CDNA sequence enco
10	20	0.8	1173	21 AAC43163	Arabidopsis thalia
11	20	0.8	1695	21 AAC49051	Arabidopsis thalia

## ALIGNMENTS

RESULT 1

AAX08517

ID AAX08517 standard; DNA: 2650 BP.

XX AC AAX08517:

DT 19-JUL-1999 (first entry)

XX

DE Poppy cytochrome P450 reductase.

XX

KW Opium poppy; alkaloids; cytochrome P450 reductase; morphine;

KW codeine; oripavine; thebaine; transformation; crop yield; probe;

KW primer; ss.

XX

OS Papaver somniferum.

XX

FH Key Location/Qualifiers

CDS 124..2175

FT /\*tag= a

FT /product= "Cytochrome P450 reductase"

XX

PN WO9911765-A1.

XX

PD 11-MAR-1999.

XX

PF 28-AUG-1998; 98WO-AU00705.

XX

PR 29-AUG-1997; 97AU-0008872.

XX

PA (JOHJ ) JOHNSON & JOHNSON RES PTY LTD.

XX

PI Atkins DG, Fist AJ, Kutchan TM, Zenk MH;

XX

DR WPI: 1998-214703/18.

Arabidopsis thalia

Poppy cytochrome p

Maize PCNA p120 ge

Mouse cDNA encodin

Human secreted exp

Neospora caninum a

Arabidopsis thalia

Arabidopsis thalia

Nucleotide sequenc

CDNA encoding enzy

Streptococcus pneu

A novel pros polyn

Human cervical can

Streptococcus pneu

Human cDNA sequenc

Human secreted pro

DNA encoding a S.

Human cDNA encodin

Senescence-associa

Human secreted pro

Human cancer assoc

S. pneumoniae deri

Streptococcus pneu

Mouse prion protei

Mouse PrP/human ta

NIDDM1 region incl

Polymorphic repeat

DNA encoding prope

DNA encoding prope

DNA encoding prope

Conus lynceus cona

Conus lynceus cona

DR P-PSDB; AAW85680, AAW85682.  
XX Nucleic acid encoding cytochrome P-450 reductase from poppy  
PT Claim 3; Fig 9a; 58pp; English.  
XX  
CC Transforming plants with a nucleic acid molecule encoding cytochrome  
CC P450 reductase alters the yield and/or type of alkaloids produced.  
CC In opium poppies it specifically increases the yield of medically  
CC useful alkaloids such as morphine, codeine, oripavine and thebaine.  
CC Sequences complementary to the coding sequence of cytochrome P450  
CC reductase are useful as probes, primers and antisense sequences, or  
CC for design of ribozymes. Transformation with DNA encoding the  
CC cytochrome P450 reductase allows regulation of the total alkaloid  
CC content and of the relative proportions of individual alkaloids.  
CC produced. Increasing the alkaloid content of poppy straw should  
CC reduce the cost of alkaloid production. Cytochrome P450 reductase  
CC is the rate-limiting enzyme in biosynthesis of alkaloids in poppies.  
CC Peptide fragments of the cytochrome P450 reductase are described in  
CC AAW85672-W85678.  
XX  
SQ Sequence 2650 BP; 766 A; 514 C; 606 G; 764 T; 0 other;  
  
Query Match 96.1%; Score 2547; DB 20; Length 2650;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2647; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 cggcacgagctgttagtatcttctaggggttgaaagaagcacagggagagcaaaagt 60  
Db 1 cggcacgagctgttagtatcttctaggggttgaaagaagcacagggagagcaaaagt 60  
  
Qy 61 cgaatctacttgaatacattcgattgcttctctctgttttaagcttcagagctctcgcta 120  
Db 61 cgaatctacttgaatacattcgattgcttctctctgttttaagcttcagagctctcgcta 120  
  
Qy 121 attatgggttcgaataattagtaattcgattgaatcgatggttaggaataatcaatgga 180  
Db 121 attatgggttcgaataattagtaattcgattgaatcgatggttaggaataatcaatgga 180  
  
Qy 181 tcagaataatttctgacccaattttcattatggttcacaaactgtagcttcaatgctgatt 240  
Db 181 tcagaataatttctgacccaattttcattatggttcacaaactgtagcttcaatgctgatt 240  
  
Qy 241 ggatttgggttcttcgatgatgataaatcttcgtctcttcataatcaaaacctattgaaact 300  
Db 241 ggatttgggttcttcgatgatgataaatcttcgtctcttcataatcaaaacctattgaaact 300  
  
Qy 301 tataaaccataattgataaagaagaagagagattgaagtgtgatcctcgtgataaattaag 360  
Db 301 tataaaccataattgataaagaagaagagagattgaagtgtgatcctcgtgataaattaag 360  
  
Qy 361 ctcaactatatttttggactcagactggttactgctgaagatttgcataaggcattggcca 420  
Db 361 ctcaactatatttttggactcagactggttactgctgaagatttgcataaggcattggcca 420  
  
Qy 421 gaagaataaaggcaagtcacaagaagcagttgtttaaagtagttgacctggatgactat 480  
Db 421 gaagaataaaggcaagtcacaagaagcagttgtttaaagtagttgacctggatgactat 480  
  
Qy 481 gcagccgagatgatcaatatgaagagaaaataaagaagagctcttgggttttttcagt 540  
Db 481 gcagccgagatgatcaatatgaagagaaaataaagaagagctcttgggttttttcagt 540  
  
Qy 541 gtgaccttattatggttggagcccaactgacaatctcgcagatttttacaaatgggttc 600  
Db 541 gtgaccttattatggttggagcccaactgacaatctcgcagatttttacaaatgggttc 600  
  
Qy 601 actcaggaacatgaaggggagagtgcttcagcaactaacttatggttttgggttg 660  
Db 601 actcaggaacatgaaggggagagtgcttcagcaactaacttatggttttgggttg 660  
  
Qy 661 ggtaacggtcaatcagcagcatttcaacaagatcgcggttagatggtgagcaactcgggt 720

Db 661 ggtaacggtcaatcagcagcatttcaacaagatcgcggttagatggtgagcaactcgggt 720  
Qy 721 aacaaggtgcaaaagcgcatgtttcaagtggggctcggtgacgatgatcaatgattgaa 780  
Db 721 aacaaggtgcaaaagcgcatgtttcaagtggggctcggtgacgatgatcaatgattgaa 780  
  
Qy 781 gatattttactgcttggcgagaattgttggactgaattggatggatcagttcctcaaaagt 840  
Db 781 gatattttactgcttggcgagaattgttggactgaattggatggatcagttcctcaaaagt 840  
  
Qy 841 gagatgctgctctcctcagtggtcacaccgtatatgtctactgttctcctgaatacagggtta 900  
Db 841 gagatgctgctctcctcagtggtcacaccgtatatgtctactgttctcctgaatacagggtta 900  
  
Qy 901 gtgatttcacgaactaaggtcgcggctcgtgatgataaacacataaatactgctaacggc 960  
Db 901 gtgatttcacgaactaaggtcgcggctcgtgatgataaacacataaatactgctaacggc 960  
  
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Db 961 gatgttcatttgatatcttccatctccttgcagaacctgtgttgcacaagaagagctc 1020  
  
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Db 1021 cacaaccccaagctctgatagatcctgtatcacatctggaggttcgacatatcaggtctctcc 1080  
  
Qy 1081 cttacatatgagactggagatcattgttgggttttatgtcgtgagaactcgatgaaactgtc 1140  
Db 1081 cttacatatgagactggagatcattgttgggttttatgtcgtgagaactcgatgaaactgtc 1140  
  
Qy 1141 gagaagcaggaaagctgttgggttcaacccctggatttgcgttttttcaattcacacggat 1200  
Db 1141 gagaagcaggaaagctgttgggttcaacccctggatttgcgttttttcaattcacacggat 1200  
  
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Db 1201 aaagaagaagggttcacccacagggaagctcattaccacctcttctccaggtccttgcacc 1260  
  
Qy 1261 ttacgatctgccttagcacgctatgctgatttttgaatcctcctagaaaggtctctctg 1320  
Db 1261 ttacgatctgccttagcacgctatgctgatttttgaatcctcctagaaaggtctctctg 1320  
  
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Db 1321 attgctctgcgctcagctatgctgtaccagtgaaagcagagagattgcgctttttgtcca 1380  
  
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Db 1381 tcacctctgggaagaatgagatttcaaaatgggttagttggaagtacagaggagctttttg 1440  
  
Qy 1441 gagatcatggccgagtttccatcagcaaaacccctcttgggtgttcttctgtcgcagta 1500  
Db 1441 gagatcatggccgagtttccatcagcaaaacccctcttgggtgttcttctgtcgcagta 1500  
  
Qy 1501 gccctcgtctaacgcctcgatactattctatctcactcctcctcctaagtgttgcctccca 1560  
Db 1501 gccctcgtctaacgcctcgatactattctatctcactcctcctcctaagtgttgcctccca 1560  
  
Qy 1561 agaattcctgtgacgctgtgcttttagtataatggttcaaaagccctacccggaaggttcaccca 1620  
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Qy 1621 ggaagtgttgcacatggaatgaacatgacgttccctcaggtagctgggctcctctattttt 1680  
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Db 1681 gttcgaacgtcaaaacttcaagtaccagctaacctcctcaactcaattatcatggtggga 1740  
  
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Db 1801 aatggtctcaactgcccagcagctctcttttcgagtaggaatcgtaatatgac 1860  
Qy 1861 ttcatttatgaacgaaactaaacaaacttcgttgaaagagagcatttcggagctagt 1920  
Db 1861 ttcatttatgaacgaaactaaacaaacttcgttgaaagagagcatttcggagctagt 1920  
Qy 1921 atgcccctttcacgtgaagggggaaagaaagaaatatattcaacataagatgagagaaa 1980  
Db 1921 atgcccctttcacgtgaagggggaaagaaagaaatatattcaacataagatgagagaaa 1980  
Qy 1981 gcaacgagatgatggaatgtagatcaggggagcgtttatctctatgtgtgtggtgatgcc 2040  
Db 1981 gcaacgagatgatggaatgtagatcaggggagcgtttatctctatgtgtgtggtgatgcc 2040  
Qy 2041 aagggaaatgccagagatgtccatcgcaagtgtgcataccattgccaaagaaacaggagccc 2100  
Db 2041 aagggaaatgccagagatgtccatcgcaagtgtgcataccattgccaaagaaacaggagccc 2100  
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Db 2461 caacactgaaacagatattagctataccaaacaaagttatgcaagaaacacaaactagta 2520  
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Db 2581 tctctgtttcttattggtctccgagagagtagtatattaatgcatttagattttgagaaaa 2640  
Qy 2641 aaaaaaaaaa 2649  
Db 2641 aaaaaaaaaa 2649

RESULT 2  
AAQ51236  
ID AAQ51236 standard; cDNA; 2114 BP.  
XX AC  
XX AAQ51236;  
DT 11-MAY-1994 (first entry)  
XX Plant NADPH cytochrome P450 reductase (ara B).  
XX

KW NADPH cytochrome P450 reductase; functional complementation;  
KW Identification; ss.  
XX Arabidopsis thaliana.  
OS  
FH Key Location/Qualifiers  
FT CDS 36..2114  
FT /tag= a  
FT /product= NADPH cytochrome P450 reductase.  
FT misc\_difference 510..512  
FT /tag= c  
FT /transl\_except= AGA encodes Lys.  
FT misc\_difference 543..545  
FT /tag= d  
FT /transl\_except= CGG encodes Lys.  
FT misc\_difference 663..665  
FT /tag= e  
FT /transl\_except= CGT encodes Lys.  
FT misc\_difference 819..821  
FT /tag= f  
FT /transl\_except= CGG encodes Lys.  
FT misc\_difference 915..917  
FT /tag= g  
FT /transl\_except= AGG encodes Lys.  
FT misc\_difference 1203..1205  
FT /tag= j  
FT /transl\_except= AGA encodes Lys.  
FT misc\_difference 1230..1232  
FT /tag= k  
FT /transl\_except= CGA encodes Lys.  
FT misc\_difference 1431..1433  
FT /tag= l  
FT /transl\_except= CGT encodes Lys.  
FT misc\_difference 1443..1445  
FT /tag= m  
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FT misc\_difference 1533..1535  
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FT misc\_difference 1623..1625  
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FT /transl\_except= CGA encodes Lys.  
FT misc\_difference 1704..1706  
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FT /transl\_except= AGA encodes Lys.  
FT misc\_difference 1782..1784  
FT /tag= p  
FT /transl\_except= AGA encodes Lys.  
FT misc\_difference 1788..1790  
FT /tag= q  
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FT misc\_difference 1872..1874  
FT /tag= r  
FT /transl\_except= CGT encodes Lys.  
FT misc\_difference 1992..1994  
FT /tag= s  
FT /transl\_except= AGG encodes Lys.  
FT misc\_difference 2004..2006  
FT /tag= t  
FT /transl\_except= CGA encodes Lys.  
FT misc\_difference 2091..2093  
FT /tag= u  
FT /transl\_except= AGA encodes Lys.  
FT misc\_difference 2100..2102

FT /\*tag= v  
 FT /transl\_except= AGA encodes Lys.

PN WO9321326-A.

XX 28-OCT-1993.

XX 13-APR-1993; 93WO-FR00367.

XX 13-APR-1992; 92FR-0004491.

XX (ORSA-) ORSAN.

XX Kazmaier M, Lacroute F, Mignotte-vieux C, Minet M;

PI Pompon D;

XX WPI; 1993-351736/44.

DR P-PSDB; AAR43581.

XX New DNA encoding plant NADPH cytochrome P450 reductase - cloned  
 PT by functional complementation in yeast, also recombinant enzyme  
 PT useful in P450 mediated bioconversion processes

XX Claim 11; Figure 9; 79pp; French.

PS A new method for determining whether a DNA sequence encodes an NADPH  
 CC cytochrome P450 reductase involves transforming yeasts with plasmids  
 CC of a total cDNA bank of plant(s). The yeasts used in the procedure  
 CC are incapable of producing their own NADPH cytochrome P450  
 CC reductase. They are then exposed to a cytochrome P450 inhibitor at a  
 CC level which is lethal to the yeast cells but not to cells which,  
 CC because of the transformation, now contain an active NADPH  
 CC cytochrome P450 reductase. Surviving clones are then isolated and  
 CC plasmid DNA extracted. The gene is inserted into the plasmid at a  
 CC site which places it under the control of an inducible promoter.

XX Sequence 2114 BP; 603 A; 400 C; 542 G; 569 T; 0 other;

Query Match 1.0%; Score 26; DB 14; Length 2114;

Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1954 tatgttcaacataagatgatggagaa 1979

|||||

Db 1893 tatgttcaacataagatgatggagaa 1918

RESULT 3

AAC98382

ID AAC98382 standard; cDNA; 600 BP.

XX AAC98382;

XX 09-MAR-2001 (first entry)

XX Human colon cancer antigen nucleotide sequence SEQ ID NO:392.

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KW identification; cytostatic; cardioactive; neuroprotective; vulnary;  
 KW immunomodulatory; muscular; gynaecological; gastrointestinal;  
 KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;  
 KW neural disorder; immune system disorder; muscular disorder;  
 KW reproductive disorder; gastrointestinal disorder; renal disorder;  
 KW infectious disease; cardiovascular disorder; ss.

XX Homo sapiens.

XX WO200055351-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05883.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2000-587534/55.

DR P-PSDB; AAB53625.

XX Colon cancer associated gene sequences, referred to as colon cancer  
 PT antigens, useful for the treatment, prevention, and diagnosis of colon  
 PT disorders such as colon cancer -

XX Claim 1; Page 856; 2104pp; English.

XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,  
 CC called human colon cancer antigens, given in AAB53234 to AAB54006. The  
 CC human colon cancer antigens can have cytostatic, cardioactive, muscular;  
 CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and  
 CC vulnary, nephrotropic, antiinfective and antibacterial activities, and  
 CC can be used in gene therapy. The colon cancer antigen polynucleotides,  
 CC proteins and antibodies to the proteins are useful for the prevention,  
 CC treatment and diagnosis of colon disorders, such as colon cancer. The  
 CC polynucleotides may be used in diagnostics and research, such as for  
 CC chromosome identification, and as hybridisation probes. The proteins  
 CC may also be used to prevent diseases such as neural disorders, immune  
 CC system disorders, muscular disorders, reproductive disorders,  
 CC gastrointestinal disorders, wounds, renal disorders, infectious  
 CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and  
 CC AAB54007 represent sequences used in the exemplification of the present  
 CC invention.

XX Sequence 600 BP; 194 A; 128 C; 140 G; 131 T; 7 other;

Query Match 0.8%; Score 22; DB 21; Length 600;

Best Local Similarity 100.0%; Pred. No. 2.2;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 498 atatgaagagaaattaaagaaa 519

|||||

Db 435 atatgaagagaaattaaagaaa 456

RESULT 4

AAQ83525

ID AAQ83525 standard; DNA; 4507 BP.

XX AC AAQ83525;

XX 22-SEP-1995 (first entry)

XX SABP gene.

XX SABP; sialic acid binding protein; binding domain; merozoite;  
 KW malaria; therapy; vaccine; ss.

XX Plasmodium falciparum.

XX WO9507353-A.

XX 16-MAR-1995.

XX 07-SEP-1994; 94WO-US10230.

XX 10-SEP-1993; 93US-0119677.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Chitnis C, Miller LH, Peterson DS, Sim KL, Su X;

PI Wellens TE;

XX

DR WPI: 1995-123427/16.  
 DR P-PSDB; AAR70232.  
 XX  
 XX New erythrocyte binding domain polypeptide(s) - isolated from  
 PT Plasmodium binding proteins, used in diagnosis, treatment and  
 PT prevention of malaria  
 XX  
 XX Disclosure: Page 39-41; 81pp; English.  
 XX  
 XX Sequences from the SABB gene (given in AA083525) were PCR amplified,  
 CC expressed on the surface of COS cells and tested for erythrocyte  
 CC binding to identify the binding domain polypeptide. A pref. SABB  
 CC binding domain comprises residues 1 to about 616 of the SABB protein  
 CC (AAR70232). Recombinant binding domain was expressed in E. coli,  
 CC yeast, mammalian, insect, and in vaccinia virus and adenovirus-  
 CC infected cells. It provides protection against P. falciparum.  
 XX  
 XX Sequence 4507 BP; 1955 A; 458 C; 796 G; 1298 T; 0 other;  
 SQ

Query Match 0.8%; Score 21; DB 16; Length 4507;  
 Best Local Similarity 100.0%; Pred. No. 6.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1987 gatgtatggaatgtgatca 2007  
 |||||  
 Db 1853 gatgtatggaatgtgatca 1873

RESULT 5  
 AAT72888  
 ID AAT72888 standard; DNA; 4507 BP.  
 XX  
 XX AC AAT72888;  
 XX  
 XX DT 11-SEP-1997 (first entry)  
 XX  
 XX Sialic acid binding protein coding sequence.  
 DE  
 DE DBL gene family; SABB; sialic acid binding protein; merozoite; malaria;  
 KW Duffy antigen binding protein; DABP; erythrocyte; var-1; var-2; var-3;  
 KW var-7; vaccine; therapy; immune response; Plasmodium; ss.  
 KW  
 XX Plasmodium falciparum.  
 OS  
 XX Key Location/Qualifiers  
 FH 56..4363  
 FT CDS /\*tag= a  
 FT /product= Duffy antigen binding protein  
 FT  
 XX WO9640766-A2.  
 XX  
 XX 19-DEC-1996.  
 XX  
 XX 07-JUN-1996; 96WO-US09508.  
 XX  
 XX 07-JUN-1995; 95US-0487826.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Chitnis C, Miller LH, Peterson DS, Sim KL, Su X;  
 PI Wellem's TE;  
 XX  
 XX WPI: 1997-052231/05.  
 DR P-PSDB; AAW22477.  
 DR  
 XX New malaria vaccines - contains cysteine-rich DBL family protein  
 PT binding domains homologous domains of the Duffy and sialic acid  
 PT binding proteins  
 XX  
 XX Example 1; Page 35-36; 96pp; English.  
 PS  
 XX This sequence represents the full length coding sequence for the sialic

CC acid binding protein (SABB). SABB and the Duffy antigen binding protein  
 CC (DABP) are soluble proteins that appear in the culture supernatant after  
 CC infected erythrocytes release merozoites. DABP and SABB mediate the  
 CC binding of merozoites and schizonts to the erythrocyte surface. These  
 CC proteins are necessary for erythrocyte invasion by the parasite. This  
 CC sequence can be used in the compositions of the invention. The  
 CC compositions are for the treatment and prevention of malaria, and  
 CC comprise either a nucleotide sequence or encoded polypeptide of the  
 CC var-1, var-2, var-3 or var-7 genes of the DBL gene family, a family of  
 CC genes having homology with conserved regions of DABP and SABB. The  
 CC compositions are used for the treatment and prevention of malaria. They  
 CC are also used in the preparation of vaccines for inducing a protective  
 CC immune response in a mammal to Plasmodium merozoites (especially  
 CC Plasmodium falciparum or Plasmodium vivax).  
 XX  
 XX Sequence 4507 BP; 1955 A; 458 C; 796 G; 1298 T; 0 other;  
 SQ

Query Match 0.8%; Score 21; DB 18; Length 4507;  
 Best Local Similarity 100.0%; Pred. No. 6.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1987 gatgtatggaatgtgatca 2007  
 |||||  
 Db 1853 gatgtatggaatgtgatca 1873

RESULT 6  
 AAZ98282  
 ID AAZ98282 standard; DNA; 4507 BP.  
 XX  
 XX AC AAZ98282;  
 XX  
 XX DT 13-JUN-2000 (first entry)  
 XX  
 XX P. falciparum SABB binding domain polypeptide encoding DNA.  
 DE  
 XX DBL gene; Duffy-binding like gene; ebl-1; Duffy Antigen Binding Protein;  
 KW DABP; Sialic Acid Binding Protein; SABB; malaria; vaccine; immunisation;  
 KW protozoacide; ds.  
 KW  
 XX Plasmodium falciparum.  
 OS  
 XX US5993827-A.  
 PN  
 XX 30-NOV-1999.  
 PD  
 XX 07-JUN-1995; 95US-0487826.  
 PF  
 XX 10-SEP-1993; 93US-0119677.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Sim KL, Chitnis C, Peterson DS, Su X, Wellem's TE, Miller LH;  
 PI WPI: 2000-194198/17.  
 DR P-PSDB; AAY77900.  
 DR  
 XX Isolated protein binding domains from Plasmodium vivax and Plasmodium  
 PT falciparum erythrocyte binding proteins useful for vaccinating against  
 PT malaria -  
 PT  
 XX Example 1; Columns 39-44; 93pp; English.  
 PS  
 XX The invention relates to ebl-1 polypeptides that are encoded by the DBL  
 CC (Duffy-binding like) gene family. The ebl-1 proteins are substantially  
 CC identical to the Duffy Antigen Binding Protein (DABP) and Sialic Acid  
 CC Binding Protein (SABB), which are soluble proteins that appear in the  
 CC culture supernatant after erythrocytes infected with malaria release  
 CC merozoites. Immunochemical studies indicate that DABP and SABB are the  
 CC respective ligands for Plasmodium vivax and Plasmodium falciparum Duffy  
 CC and sialic acid receptors on erythrocytes. The ebl-1 polypeptides may be  
 CC used to vaccinate against malaria, especially caused by P. falciparum.

CC Immunization with the polypeptide provides effective protection against  
CC malaria. The present sequence represents the SAPP binding domain  
CC polypeptide encoding DNA.

XX Sequence 4507 BP; 1955 A; 458 C; 796 G; 1298 T; 0 other;

Query Match 0.8%; Score 21; DB 21; Length 4507;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1987 gatgtatggaatgtgatca 2007  
|||||  
Db 1853 gatgtatggaatgtgatca 1873

## RESULT 7

AAC74719  
ID AAC74719 standard; cDNA; 306 BP.

XX AAC74719;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF274 polynucleotide sequence SEQ ID NO:547.

XX Human: open reading frame; ORFX: detection; cytostatic; hepatotropic;  
KW vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KW thrombosis; contraceptive; ss.

XX Homo sapiens.

OS WO200058473-A2.

PN 05-OCT-2000.

PD 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI: 2000-602362/57.

DR P-PSDB; AAB40510.

XX Novel nucleic acids and peptides derived from open reading frame X,  
PT useful for treating e.g. cancers, proliferative disorders,  
PT neurodegenerative disorders and cardiovascular disease -

FS Claim 5; Page 707; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;  
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;  
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;

CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;  
CC antithyroid; and antianaemic. The sequences can be used for determining  
CC the presence of or predisposition to, or preventing or treating  
CC pathological conditions associated with an ORFX-associated disorder. The  
CC nucleic acids can be used to express ORFX proteins in gene therapy  
CC vectors. The proteins and nucleic acids may be used to treat cancers,  
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
CC graft vs host disease, cardiovascular disease, diabetes mellitus, lupus  
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 306 BP; 80 A; 59 C; 55 G; 101 T; 11 other;

Query Match 0.8%; Score 20; DB 21; Length 306;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1634 catggatgaagcatgcagtt 1653  
|||||  
Db 36 catggatgaagcatgcagtt 55

## RESULT 8

AAC35800

ID AAC35800 standard; DNA; 485 BP.

XX AAC35800;

XX 17-OCT-2000 (first entry)

DE Zea mays DNA fragment SEQ ID NO: 11470.

KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic;  
KW pathway; promoter; termination sequence; corn; ss.

XX Zea mays subsp. mays.

PN EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR	14-MAY-1999;	99US-0134218.
PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134768.
PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135353.
PR	24-MAY-1999;	99US-0135629.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137502.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
PR	10-JUN-1999;	99US-0138847.
PR	14-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
PR	16-JUN-1999;	99US-0139453.
PR	17-JUN-1999;	99US-0139492.
PR	18-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
PR	18-JUN-1999;	99US-0139456.
PR	18-JUN-1999;	99US-0139457.
PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
PR	18-JUN-1999;	99US-0139460.
PR	18-JUN-1999;	99US-0139461.
PR	18-JUN-1999;	99US-0139462.
PR	18-JUN-1999;	99US-0139463.
PR	18-JUN-1999;	99US-0139750.
PR	18-JUN-1999;	99US-0139763.
PR	21-JUN-1999;	99US-0139817.
PR	22-JUN-1999;	99US-0139899.
PR	23-JUN-1999;	99US-0140353.
PR	23-JUN-1999;	99US-0140354.
PR	24-JUN-1999;	99US-0140695.
PR	24-JUN-1999;	99US-0140823.
PR	29-JUN-1999;	99US-0140991.
PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142803.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144334.
PR	19-JUL-1999;	99US-0144335.
PR	20-JUL-1999;	99US-0144352.
PR	20-JUL-1999;	99US-0144632.
PR	20-JUL-1999;	99US-0144884.
PR	21-JUL-1999;	99US-0144814.
PR	21-JUL-1999;	99US-0145086.
PR	21-JUL-1999;	99US-0145088.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145918.
PR	27-JUL-1999;	99US-0145919.
PR	28-JUL-1999;	99US-0145951.
PR	02-AUG-1999;	99US-0146386.
PR	02-AUG-1999;	99US-0146388.
PR	03-AUG-1999;	99US-0146389.
PR	03-AUG-1999;	99US-0147038.
PR	04-AUG-1999;	99US-0147204.
PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.

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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match      0.8%; Score 20; DB 21; Length 485;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2032 ggtgatgcccaagggaatggc 2051
      |||||
Db 338 ggtgatgcccaagggaatggc 357

RESULT 9
AAA46546
ID AAA46546 standard; cDNA; 531 BP.
XX
XX AC AAA46546;
XX
XX DT 25-SEP-2000 (first entry)
XX
DE cDNA sequence encoding a potassium channel interactor polypeptide.
XX
XX KW Potassium channel interactor; PCIP; potassium channel; epilepsy;
XX KW spinocerebellar ataxia; nervous system disorder; cardiovascular disorder;
XX KW transient outward current; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT CDS 1..339
XX FT /*tag= a
XX FT /product= "potassium channel interactor"
XX
XX PN WO200031133-A2.
XX
XX PD 02-JUN-2000.
XX
XX PF 19-NOV-1999; 99WO-US27428.
XX
XX 20-NOV-1998; 98US-0109333.
XX 25-NOV-1998; 98US-0110033.
XX 30-NOV-1998; 98US-0110277.
XX 23-APR-1999; 99US-0298731.
XX 09-JUL-1999; 99US-0350614.
XX 09-JUL-1999; 99US-0350874.
XX 21-SEP-1999; 99US-0399913.
XX 21-SEP-1999; 99US-0400492.
XX
XX (MILL) MILLENNIUM PHARM INC.
XX (AMHP) AMERICAN HOME PROD CORP.
XX
XX Rhodes K, Betty M, Ling H, An W;
XX
XX WPI: 2000-400043/34.
XX P-PSDB: AAY93480.
XX
XX New polynucleotide with homology to the sequence encoding phosphate
XX channel interacting protein useful in the treatment of e.g. epilepsy
XX and spinocerebellar ataxia -
XX
XX Claim 2; Fig 19; 306pp; English.
XX
XX The present sequence encodes a potassium channel interactor protein
XX (PCIP). The PCIP polypeptides bind to a potassium channel, modulate
CC
```

```
CC the activity of a potassium channel protein, and/or modulate a potassium
CC channel mediated activity in a cell. The polynucleotides and
CC polypeptides are useful in the treatment of epilepsy, and
CC spinocerebellar ataxia, as well as nervous system related disorders and
CC cardiovascular disorders associated with abnormal transient outward
CC currents. They are also useful for identifying compounds which can
CC bind to and modulate the expression and function of the PCIP nucleic
CC acid molecules, and proteins.
XX
XX SQ Sequence 531 BP; 174 A; 120 C; 115 G; 121 T; 1 other;

Query Match      0.8%; Score 20; DB 21; Length 531;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2630 ttttgagaaaaa 2649
      |||||
Db 499 ttttgagaaaaa 518

RESULT 10
AAC43163/c
ID AAC43163 standard; DNA; 1173 BP.
XX
XX AC AAC43163;
XX
XX DT 17-OCT-2000 (first entry)
XX
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38259.
XX
XX KW Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway;
XX KW metabolic pathway; promoter; termination sequence; ss.
XX
XX OS Arabidopsis thaliana.
XX
XX PN EPI033405-A2.
XX
XX PD 06-SEP-2000.
XX
XX PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 23-APR-1999; 99US-0130891.
XX 28-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.
XX 04-MAY-1999; 99US-0132484.
XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 06-MAY-1999; 99US-0132487.
XX 07-MAY-1999; 99US-0132863.
XX 11-MAY-1999; 99US-0134256.
XX 14-MAY-1999; 99US-0134218.
XX 14-MAY-1999; 99US-0134219.
XX 14-MAY-1999; 99US-0134221.
XX 14-MAY-1999; 99US-0134370.
XX 18-MAY-1999; 99US-0134768.
XX 19-MAY-1999; 99US-0134941.
XX 20-MAY-1999; 99US-0135124.
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PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
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PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
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PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.

PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151066.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 0.8%; Score 20; DB 21; Length 2136;  
Best Local Similarity 100.0%; Pred. No. 19;  
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Qy 1093 actggagatcatgttgggtgt 1112  
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Db 1042 actggagatcatgttgggtgt 1061

RESULT 13  
AA08520  
ID AAX08520 standard; DNA; 2558 BP.  
XX  
AC AAX08520;  
XX  
DT 19-JUL-1999 (first entry)  
XX  
DE Poppy cytochrome P450 reductase.  
XX  
KW Opium poppy; alkaloids; cytochrome P450 reductase; morphine;  
KW codeine; oripavine; thebaine; transformation; crop yield; probe;  
KW primer; ss.  
XX  
OS Eschscholzia californica.  
XX  
FH Key Location/Qualifiers  
FT CDS 127..2241  
FT /\*tag= a  
FT /product= "Cytochrome P450 reductase"  
XX  
PN W09911765-A1.  
XX  
PD 11-MAR-1999.  
XX  
PF 28-AUG-1998; 98WO-AU00705.  
XX  
PR 29-AUG-1997; 97AU-0008872.  
XX  
PA (JOHJ ) JOHNSON & JOHNSON RES PTY LTD.  
XX  
PI Atkins DG, Fist AJ, Kutchan TM, Zenk MH;  
XX  
DR WPI; 1999-214703/18.  
DR P-PSDB; AAW85681, AAW85683.  
XX  
PT Nucleic acid encoding cytochrome P-450 reductase from poppy  
XX  
PS Claim 3; Fig 9b; 58pp; English.  
XX  
CC Transforming plants with a nucleic acid molecule encoding cytochrome  
CC P450 reductase alters the yield and/or type of alkaloids produced.  
CC In opium poppies it specifically increases the yield of medically  
CC useful alkaloids such as morphine, codeine, oripavine and thebaine.  
CC Sequences complementary to the coding sequence of cytochrome P450  
CC reductase are useful as probes, primers and antisense sequences, or  
CC for design of ribozymes. Transformation with DNA encoding the  
CC cytochrome P450 reductase allows regulation of the total alkaloid  
CC content and of the relative proportions of individual alkaloids.  
CC produced. Increasing the alkaloid content of poppy straw should  
CC reduce the cost of alkaloid production. Cytochrome P450 reductase  
CC is the rate-limiting enzyme in biosynthesis of alkaloids in poppies.  
CC Peptide fragments of the cytochrome P450 reductase are described in  
CC AAW85672-W85678.  
XX  
SQ Sequence 2558 BP; 750 A; 477 C; 592 G; 739 T; 0 other;

Query Match 0.8%; Score 20; DB 20; Length 2558;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 860 ctgaattggtcagttgctc 879

RESULT 14  
AAA26994  
ID AAA26994 standard; DNA; 2792 BP.  
XX  
AC AAA26994;  
XX

DT 22-AUG-2000 (first entry)  
XX  
DE Maize PCNA P120 gene fragment #3.  
XX  
KW Maize; plant cell proliferation-associated protein;  
KW proliferating cell nuclear antigen; cell division stimulation;  
KW proliferative; transgenic plant; plant growth; co-suppression;  
KW chimeric gene; ss.  
XX  
OS Zea mays.  
XX  
FH Key Location/Qualifiers  
FT CDS 2..2479  
FT /\*tag= a  
FT /partial  
FT /product= "PCNA P120"  
XX  
PN W0200031269-A2.  
XX  
PD 02-JUN-2000.  
XX  
PF 19-NOV-1999; 99WO-US27550.  
XX  
PR 20-NOV-1998; 98US-0109266.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Cahoon RE, Klein TM, Weng Z, Lowe KS;  
XX  
DR WPI; 2000-400079/34.  
DR P-PSDB; AAY94310.  
XX  
PT Nucleic acids encoding proteins involved in plant cell division and  
PT proliferation useful for identifying modulators of plant growth -  
XX  
PS Claim 2; Page 36-37; 43pp; English.  
XX  
CC The present sequence is a nucleic acid fragment which encodes  
CC proliferating cell nuclear antigen (PCNA) P120, a plant cell  
CC proliferation-associated protein from Zea mays. The entire sequence  
CC was found in a clone designated p0115.cisme95r from a cDNA library made  
CC from corn leaf and sheath meristem tissue. Chimeric genes containing the  
CC present nucleic acid fragment can be introduced into monocots and dicots  
CC to produce plants expressing transgenic PCNA P120. By choosing a suitable  
CC promoter, the fragment can be overexpressed or expressed at certain  
CC developmental stages or in certain tissues. Co-suppression or antisense  
CC chimeric genes can also be introduced to produce plants with reduced or  
CC eliminated gene expression, thus inhibiting cell division and  
CC proliferation. The present sequence may also be used to transform E. coli  
CC in order to produce high levels of the protein for analysis. The nucleic  
CC acid and the protein it encodes may be used to stimulate plant growth and  
CC cell division and proliferation and to identify modulators of cell  
CC division and proliferation.  
XX  
SQ Sequence 2792 BP; 841 A; 511 C; 691 G; 749 T; 0 other;

Query Match 0.8%; Score 20; DB 21; Length 2792;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2630 ttgtgagaaaaa 2649  
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Db 2757 ttgtgagaaaaa 2776

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XX  
AC AAS11602;  
XX

Search completed: December 27, 2001, 15:59:40  
Job time: 6445 sec

DT 24-OCT-2001 (first entry)  
XX DE Mouse cDNA encoding CRIM1 protein.  
XX  
XX CRIM-1; Mouse; human chromosome 2p21-16.3; ophthalmological;  
KW neuroprotective; renal; osteopathic; dental; vulnerary; immunogen;  
KW antibody; gene therapy; neurodegenerative disease; eye disorder;  
KW cataract; bone morphogenic protein; BMG; renal disease; bone abnormality;  
KW tooth abnormality; wound; ss; S52.  
XX  
OS Mus sp.  
XX  
XX  
XX Key Location/Qualifiers  
FH 63...3175  
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FT /\*product= "CRIM1"  
FT sig\_peptide 63...89 /\*tag= b  
FT mat\_peptide 90...3172 /\*tag= c  
FT /\*label= Mature\_CRIM1  
XX  
XX WO200138519-A1.  
XX  
XX  
XX 31-MAY-2001.  
XX  
XX PF 24-NOV-2000; 2000WO-AU01435.  
XX  
XX PR 26-NOV-1999; 99AU-0004348.  
XX  
XX (UYQU ) UNIV QUEENSLAND.  
XX  
XX PI Little M, Yamada T, Holmes G, Georgas K, Kolle G, Wilkinson L;  
XX  
XX WPI; 2001-343951/36.  
XX P-PSDB; AAU07142.  
XX  
XX Nucleic acids from human chromosome 2p21-16.3 and the encoded peptide,  
PT useful for preventing, diagnosing and treating e.g. eye disease,  
PT especially cataract formation -  
XX  
XX Claim 3; Fig 2; 169pp; English.  
XX  
XX The invention relates to nucleic acids from human chromosome 2p21-16.3  
CC and the encoded peptide (and mouse and chicken orthologues) that  
CC comprises a pEECCPLP group, an insulin-like growth factor binding protein  
CC (IGFBP)-like domain, cysteine-rich domains, an RGD (undefined) group  
CC and a transmembrane domain. The protein, e.g. CRIM1, interacts with  
CC peptides of the transforming growth factor superfamily. A composition  
CC comprising an expression construct comprising the nucleic acids of the  
CC invention or a mimetic which antagonises or mimics an activity of a CRIM1  
CC polypeptide may be used in a method for modulating the biological  
CC activity of a polypeptide of the bone morphogenic protein (BMP) family.  
CC In this way they may be used to prevent or treat an eye disease,  
CC especially cataract formation. They may also be used to treat  
CC neurodegenerative diseases, renal and kidney disease, bone and tooth  
CC abnormalities, wounds and skin damage, e.g. by use of the nucleic acid in  
CC gene therapy by using antibodies directed against CRIM1 polypeptides.  
CC The present sequence encodes mouse CRIM1 (AKA S52).  
XX  
XX Sequence 4101 BP; 967 A; 1067 C; 1154 G; 911 T; 2 other;

Query Match 0.8%; Score 20; DB 22; Length 4101;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2630 ttctgagaaaaaa 2649  
Db 4077 ttctgagaaaaaa 4096

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 13:07:50 ; Search time 82.71 Seconds  
(without alignments)  
7253.539 Million cell updates/sec

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Perfect score: 2649  
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Searched: 351203 seqs, 11328999 residues

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	0.8	4507	2	US-08-568-459A-3
2	21	0.8	4507	2	US-08-487-8268-3
C 3	19	0.7	1651	2	US-08-844-058-1
C 4	19	0.7	49136	4	US-09-422-869-1
C 5	18	0.7	379	4	US-09-142-078-57
C 6	18	0.7	379	4	US-09-357-141-57
C 7	18	0.7	394	4	US-09-142-078-53
C 8	18	0.7	394	4	US-09-357-141-53
C 9	18	0.7	580	4	US-09-142-078-49
C 10	18	0.7	580	4	US-09-357-141-49
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C 13	18	0.7	1124	2	US-09-408-257-1
C 14	18	0.7	2149	1	US-08-374-502-1
C 15	18	0.7	2886	1	US-08-073-383-3
C 16	18	0.7	2886	3	US-08-328-239A-2
C 17	18	0.7	2886	5	PCT-US94-06365-3
C 18	18	0.7	2886	5	PCT-US95-13661-2
C 19	18	0.7	2890	3	US-08-848-810-1
C 20	18	0.7	2940	1	US-08-428-415-3
C 21	18	0.7	2940	1	US-08-379-685-3
C 22	18	0.7	2940	2	US-08-854-029-3
C 23	18	0.7	2940	4	US-08-428-762-3
C 24	18	0.7	3306	1	US-08-261-206A-71
C 25	18	0.7	7070	1	US-08-619-554-3
C 26	18	0.7	18073	4	US-09-078-294-12
C 27	17	0.6	27	2	US-08-244-122-12

C 28	17	0.6	62	4	US-09-296-607-1	Sequence 1, Appl
C 29	17	0.6	63	2	US-08-776-944-10	Sequence 10, Appl
C 30	17	0.6	66	2	US-08-776-944-11	Sequence 11, Appl
C 31	17	0.6	188	1	PCT-US92-10087-2	Sequence 2, Appl
C 32	17	0.6	188	5	PCT-US92-10087-2	Sequence 2, Appl
C 33	17	0.6	607	4	US-09-328-111-531	Sequence 531, App
C 34	17	0.6	1223	2	US-08-463-081B-3	Sequence 3, Appl
C 35	17	0.6	1223	2	US-08-461-379A-3	Sequence 3, Appl
C 36	17	0.6	1223	2	US-08-462-390B-3	Sequence 3, Appl
C 37	17	0.6	1223	3	US-08-463-074B-3	Sequence 3, Appl
C 38	17	0.6	1223	3	US-08-465-585C-3	Sequence 3, Appl
C 39	17	0.6	1223	3	US-08-652-446-3	Sequence 3, Appl
C 40	17	0.6	1317	3	US-08-915-498B-36	Sequence 36, Appl
C 41	17	0.6	1662	2	US-08-956-012-2	Sequence 2, Appl
C 42	17	0.6	1668	1	US-08-463-090B-1	Sequence 1, Appl
C 43	17	0.6	1976	3	US-09-165-042-2	Sequence 2, Appl
C 44	17	0.6	2009	4	US-09-446-504-17	Sequence 17, Appl
C 45	17	0.6	2280	2	US-09-055-097-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-08-568-459A-3  
; Sequence 3, Application US/08568459A  
; Patent No. 5849306  
; GENERAL INFORMATION:  
; APPLICANT: Sim, Kim L.  
; APPLICANT: Chitnis, Chetan  
; APPLICANT: Miller, Louis H.  
; APPLICANT: Peterson, David S.  
; APPLICANT: Su, Xin-zhaun  
; APPLICANT: Wellem, Thomas E.  
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe Martens Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: California  
; COUNTRY: US  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/568,459A  
; FILING DATE: 07-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelien, Ned  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: NIH121.001CP1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 235-8550  
; TELEFAX: (619) 235-0176  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4507 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Plasmodium falciparum  
US-08-568-459A-3





QY 1764 cagaggatttctgcagga 1781  
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 Db 139 CAGAGGATTCTGCAGGA 122

Query Match 0.7%; Score 19; DB 4; Length 49136;  
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QY 41 gcacaggagagcaaaag 59  
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 Db 5275 GCACAGGAGAGCAAAAG 5257

RESULT 5  
 US-09-142-078-57/C  
 ; Sequence 57, Application US/09142078  
 ; Patent No. 6172041  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McCabe, R. Tyler  
 ; APPLICANT: Zhou, Li-Ming  
 ; APPLICANT: Layer, Richard T.  
 ; TITLE OF INVENTION: Use of Conantokins  
 ; NUMBER OF SEQUENCES: 71  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.  
 ; STREET: 555 Thirteenth Street, N.W., Suite 701-E  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/142.078  
 ; FILING DATE: 10-FEB-1999  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO US97/12652  
 ; FILING DATE: 21-JUL-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/762,377  
 ; FILING DATE: 06-DEC-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/684,750  
 ; FILING DATE: 22-JUL-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ihnen, Jeffrey L.  
 ; REGISTRATION NUMBER: 28,957  
 ; REFERENCE/DOCKET NUMBER: 2314-135.A  
 ; TELEPHONE: 202-783-6040  
 ; TELEFAX: 202-783-6031  
 ; INFORMATION FOR SEQ ID NO: 57:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 379 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (cdna)  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Conus lynceus  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..282  
 ; US-09-142-078-57

Query Match 0.7%; Score 18; DB 4; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 52;  
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QY 1764 cagaggatttctgcagga 1781  
 |||||  
 Db 139 CAGAGGATTCTGCAGGA 122

RESULT 6  
 US-09-357-141-57/C  
 ; Sequence 57, Application US/09357141  
 ; Patent No. 6277825  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: McIntosh, J. Michael  
 ; APPLICANT: McCabe, R. Tyler  
 ; APPLICANT: Layer, Richard T.  
 ; APPLICANT: Zhou, Li-Ming  
 ; TITLE OF INVENTION: Use of Conantokins for Treating Pain  
 ; FILE REFERENCE: 2314-171  
 ; CURRENT APPLICATION NUMBER: US/09/357.141  
 ; CURRENT FILING DATE: 1999-07-20  
 ; PRIOR APPLICATION NUMBER: US 09/283,277  
 ; PRIOR FILING DATE: 1999-04-01  
 ; PRIOR APPLICATION NUMBER: US 09/142,078  
 ; PRIOR FILING DATE: 1999-02-10  
 ; PRIOR APPLICATION NUMBER: WO US97/12652  
 ; PRIOR FILING DATE: 1997-07-21  
 ; PRIOR APPLICATION NUMBER: US 08/762,377  
 ; PRIOR FILING DATE: 1996-12-06  
 ; PRIOR APPLICATION NUMBER: US 08/684,750  
 ; PRIOR FILING DATE: 1996-07-22  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 57  
 ; LENGTH: 379  
 ; TYPE: DNA  
 ; ORGANISM: Conus lynceus  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(282)  
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Query Match 0.7%; Score 18; DB 4; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 139 CAGAGGATTCTGCAGGA 122

RESULT 7  
 US-09-142-078-53/C  
 ; Sequence 53, Application US/09142078  
 ; Patent No. 6172041  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McCabe, R. Tyler  
 ; APPLICANT: Zhou, Li-Ming  
 ; APPLICANT: Layer, Richard T.  
 ; TITLE OF INVENTION: Use of Conantokins  
 ; NUMBER OF SEQUENCES: 71  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.  
 ; STREET: 555 Thirteenth Street, N.W., Suite 701-E  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
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 ; COMPUTER: IBM PC compatible  
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 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/142,078  
; FILING DATE: 10-FEB-1999  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO US97/12652  
; FILING DATE: 21-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/762,377  
; FILING DATE: 06-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/684,750  
; FILING DATE: 22-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 2314-135.A  
; TELEPHONE: 202-783-6040  
; TELEFAX: 202-783-6031  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 394 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (cdna)  
; ORIGINAL SOURCE:  
; ORGANISM: Conus ochroleucus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..294  
US-09-142-078-53

Query Match 0.7%; Score 18; DB 4; Length 394;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1764 cagaggatttctgcagga 1781  
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Db 139 CAGAGGATTTCTGCAGGA 122

RESULT 8  
US-09-357-141-53/c  
; Sequence 53, Application US/09357141  
; Patent No. 6277825  
; GENERAL INFORMATION:  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: McCabe, R. Tyler  
; APPLICANT: Layer, Richard T.  
; APPLICANT: Zhou, Li-Ming  
; TITLE OF INVENTION: Use of Conantokins for Treating Pain  
; FILE REFERENCE: 2314-171  
; CURRENT APPLICATION NUMBER: US/09/357,141  
; CURRENT FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: US 09/283,277  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: US 09/142,078  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: WO US97/12652  
; PRIOR FILING DATE: 1997-07-21  
; PRIOR APPLICATION NUMBER: US 08/762,377  
; PRIOR FILING DATE: 1996-12-06  
; PRIOR APPLICATION NUMBER: US 08/684,750  
; PRIOR FILING DATE: 1996-07-22  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 53  
; LENGTH: 394  
; TYPE: DNA  
; ORGANISM: Conus ochroleucus

; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(294)  
US-09-357-141-53  
  
Query Match 0.7%; Score 18; DB 4; Length 394;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1764 cagaggatttctgcagga 1781  
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Db 139 CAGAGGATTTCTGCAGGA 122  
  
RESULT 9  
US-09-142-078-49/c  
; Sequence 49, Application US/09142078  
; Patent No. 6172041  
; GENERAL INFORMATION:  
; APPLICANT: McCabe, R. Tyler  
; APPLICANT: Zhou, Li-Ming  
; APPLICANT: Layer, Richard T.  
; TITLE OF INVENTION: Use of Conantokins  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.  
; STREET: 555 Thirteenth Street, N.W., Suite 701-E  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/142,078  
; FILING DATE: 10-FEB-1999  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO US97/12652  
; FILING DATE: 21-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/762,377  
; FILING DATE: 06-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/684,750  
; FILING DATE: 22-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 2314-135.A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-783-6040  
; TELEFAX: 202-783-6031  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 580 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (cdna)  
; ORIGINAL SOURCE:  
; ORGANISM: Conus radiatus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 127..447  
US-09-142-078-49

Query Match 0.7%; Score 18; DB 4; Length 580;  
Best Local Similarity 100.0%; Pred. No. 51;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1764 cagaggatttctgcagga 1781  
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Db 286 CAGAGGATTCTGCAGGA 269

## RESULT 10

US-09-357-141-49/C  
; Sequence 49, Application US/09357141  
; Patent No. 6277825  
; GENERAL INFORMATION:  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: McCabe, R. Tyler  
; APPLICANT: Laver, Richard T.  
; APPLICANT: Zhou, Li-Ming  
; TITLE OF INVENTION: Use of Conantokins for Treating Pain  
; FILE REFERENCE: 2314-171  
; CURRENT APPLICATION NUMBER: US/09/357,141  
; CURRENT FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: US 09/283,277  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: US 09/142,078  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: WO US97/12652  
; PRIOR FILING DATE: 1997-07-21  
; PRIOR APPLICATION NUMBER: US 08/762,377  
; PRIOR FILING DATE: 1996-12-06  
; PRIOR APPLICATION NUMBER: US 08/684,750  
; PRIOR FILING DATE: 1996-07-22  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 49  
; LENGTH: 580  
; TYPE: DNA  
; ORGANISM: Conus radiatus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (127)..(447)  
US-09-357-141-49

Query Match 0.7%; Score 18; DB 4; Length 580;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1764 cagaggatttctgcagga 1781  
|||||

Db 286 CAGAGGATTCTGCAGGA 269

## RESULT 11

US-08-578-551-1  
; Sequence 1, Application US/08578551  
; Patent No. 5854050  
; GENERAL INFORMATION:  
; APPLICANT: Dalboge, Henrik  
; APPLICANT: Christgau, Stephan  
; APPLICANT: Andersen, Lene N.  
; APPLICANT: Kofod, Lene V.  
; APPLICANT: Kauppinen, Sakari M.  
; APPLICANT: Nielsen, Jack B.  
; APPLICANT: Dammann, Claus  
; TITLE OF INVENTION: An Enzyme with Protease Activity  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 58540500 No. 58540500disk of No. 58540500th America, Inc.  
; STREET: 405 Lexington Avenue, 64th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10174-6401

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/578,551  
; FILING DATE: 01-FEB-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DK 0811/93  
; FILING DATE: 06-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO 95/02044  
; FILING DATE: 19-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lambiris, Elias J.  
; REGISTRATION NUMBER: 33,728  
; REFERENCE/DOCKET NUMBER: 4006.204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1124 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Aspergillus aculeatus  
; US-08-578-551-1

Query Match 0.7%; Score 18; DB 2; Length 1124;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2632 ttgagagagagagagagagag 2649  
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Db 1103 TTGAGAGAGAGAGAGAGAG 1120

## RESULT 12

US-09-190-982-1  
; Sequence 1, Application US/09190982  
; Patent No. 5998190  
; GENERAL INFORMATION:  
; APPLICANT: Dalboge, Henrik  
; APPLICANT: Christgau, Stephan  
; APPLICANT: Andersen, Lene N.  
; APPLICANT: Kofod, Lene V.  
; APPLICANT: Kauppinen, Sakari M.  
; APPLICANT: Nielsen, Jack B.  
; APPLICANT: Dammann, Claus  
; TITLE OF INVENTION: An Enzyme with Protease Activity  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 59981900 No. 59981900disk of No. 59981900th America, Inc.  
; STREET: 405 Lexington Avenue, 64th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/190,982

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13
US-09-408-257-1
; Sequence 1, Application US/09408257
; Patent No. 6190905
; GENERAL INFORMATION:
; APPLICANT: Dalboge, Henrik
; APPLICANT: Christgau, Stephan
; APPLICANT: Andersen, Lene N.
; APPLICANT: Kofod, Lene V.
; APPLICANT: Kauppinen, Sakari M.
; APPLICANT: Nielsen, Jack B.
; APPLICANT: Dammann, Claus
; TITLE OF INVENTION: An Enzyme with Protease Activity
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6190905o No. 6190905disk of No. 6190905th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/408,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,551
; FILING DATE: 01-FEB-1996
; APPLICATION NUMBER: DK 0811/93
; FILING DATE: 06-JUL-1993

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RESULT 14
US-08-374-502-1/c
; Sequence 1, Application US/08374502
; Patent No. 5759805
; GENERAL INFORMATION:
; APPLICANT: Feldhaus, Andrew L.
; APPLICANT: Ziegler, Steven F.
; TITLE OF INVENTION: CD69 TRANSCRIPTIONAL REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,502
; FILING DATE: 20-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER M.
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 22627-20011.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2149 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:

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; NAME/KEY: mat\_peptide  
; LOCATION: 2080  
US-08-374-502-1

Query Match 0.7%; Score 18; DB 1; Length 2149;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 tcacaactgtagcttcaa 232  
|||||  
DB 1885 TCACACTGTAGCTTCAA 1868

RESULT 15  
US-08-073-383-3  
; Sequence 3, Application US/08073383  
; Patent No. 5443962  
; GENERAL INFORMATION:  
; APPLICANT: Draetta, Giulio  
; APPLICANT: Cottarel, Guillaume  
; APPLICANT: Damagnez, Veronique  
; TITLE OF INVENTION: [fillin "Insert Title of Application" ]ASSAY AND REAGENTS FOR  
; NUMBER OF INVENTION: ANTI-PROLIFERATIVE AGENTS]  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII (text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/073,383  
; FILING DATE: 19930604  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: MII-009  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2886 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 73..1773  
US-08-073-383-3

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Best Local Similarity 100.0%; Pred. No. 47;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2632 ttgagaaaaa 2649  
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DB 2863 TTGAGAAAAA 2880

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 2649  
Sequence: 1 cggcagcagctgttagtat.....tttgagaaaaa 2649

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues  
Total number of hits satisfying chosen parameters: 2944280

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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
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35:	em_htg_rod.:	
36:	em_htg_other.:	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB ID	Description
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2	1126.4	42.5	2498	8	AF302496
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4	1094.8	41.3	2641	8	VSNER
5	987.6	37.3	2199	8	ATATRIG
6	985	37.2	2114	6	A75959
7	969.8	36.6	2561	8	ECU67186
8	918.6	34.7	2493	8	AF302497
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10	911.2	34.4	2610	8	AF302498
11	895.4	33.8	2136	8	AF325101
12	875.2	33.0	2556	8	AF024635
13	875	33.0	2290	8	ATATR2M
14	875	33.0	2423	6	A75961
15	874	33.0	2466	8	AF024634
16	873.6	33.0	2618	8	CRCPRA
17	867.4	32.7	2333	8	AF123610
18	862.4	32.6	2545	8	AF002698
19	859.8	32.5	2112	6	A75963
20	807.6	30.5	1863	6	AX082548
21	807.6	30.5	1863	8	HTU2NFR
22	659.2	24.9	1539	8	HTL2NFR
23	569.6	21.5	2312	8	AF367288
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27	203.8	7.7	3450	3	AB042615
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30	194	7.3	9476	12	CVU40578
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DEFINITION	Papaver somniferum NADPH:ferrihemoprotein oxidoreductase mRNA, complete cds.				
ACCESSION	U67185				
VERSION	U67185.1	GI:2580496			
KEYWORDS					
SOURCE	Opium poppy.				
ORGANISM	Papaver somniferum				
	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales; Papaveraceae; Papaver.				
REFERENCE	1 (bases 1 to 2650)				
AUTHORS	Rosco.A., Pauli.H.H., Priesner.W. and Kutchan.T.M.				
TITLE	Cloning and heterologous expression of NADPH-cytochrome P450 reductases from the Papaveraceae				
JOURNAL	Arch. Biochem. Biophys. 348 (2), 369-377 (1997)				
MEDLINE	98096363				
REFERENCE	2 (bases 1 to 2650)				

AUTHORS Rosco,A. and Kutchan,T.M.

TITLE Direct Submission

JOURNAL Submitted (19-AUG-1996) Laboratorium fuer Molekulare Biologie,

Universitaet Muenchen, Karlstrasse 29, Munich 80333, Germany

## FEATURES

source

Location/Qualifiers

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/organism="Papaver somniferum"

/db\_xref="taxon:3469"

/note="cell suspension culture"

124. .2175

/EC\_number="1.6.2.4"

/function="catalyzes the reduction of the

heme-thiolate-dependent monooxygenases and oxidases;

reduces cytochrome c"

/note="cytochrome P-450 reductase"

/codon\_start=1

/product="NADPH: ferrihemoprotein oxidoreductase"

/protein\_id="AAC05021.1"

/db\_xref="GI:2580497"

/translation="MGSNLANSTESMLGISIGSEYISDPIFIMVTTVASMLIGFGE

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PPRKASLIASAHASVPSEARLFLSPILGKNEYSKWVYQSORSLEIMAEFPSAKP

PLGVFPAAPRLPPRYYSISSSPKFAPSRIHVTICALYVQSPFGRVHRGVCSTWVKH

AVPFDWNAPIFRFTSNKPLADPSTPIIMVGPGLAPFRFGLQERHAKHNGAOLGP

ALVFFGCGNFIYDEELNLFVERGIVSELVIAFSREGEKKEIYVQHKMKWKATDYM

NVTSGDGYLYVCGDAKGMARDVHRTLTHIAEQEGPMESSAAEAARVKKLOVEERYLDV

W"

BASE COUNT 766 a 514 c 606 g 764 t

## ORIGIN

Query Match 99.9%; Score 2645.8; DB 8; Length 2650;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2647; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cggcagcagcttgtagtatcttcttagggtttgaagaagcacagggagagcaaaagt 60

Db 1 CGGCACGAGCTGTGTAGTATCTTCTAGGGTTTGAAGAAGCACAGGGAGAGCAAAAGT 60

Qy 61 cgaactcacttgaaatacattcgatgctctctctctgttttaagcttcagagctctcgta 120

Db 61 CGAATCTACTTGAATACATTCGATGCTTCTCTCTGTTTAAAGCTTCAGAGTCTCTGTA 120

Qy 121 attatgggttcgaataatttagtaattcgaattgaatcgatgtaggaatatcaatagga 180

Db 121 ATTATGGGTTTCGAATAATTAGCTAAATTCGATTGAATCGATGTTAGGAATATCAATAGGA 180

Qy 181 tcagaataattctgacccaattttctatgttcacaaactgtagcttcaatgctgatt 240

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Qy 241 ggaattgtttctcgcatgatataaacttcgtctctctcctcaatcaaacctattgaaact 300

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RESULT 2  
AF302496  
LOCUS  
DEFINITION Hybrid poplar (Populus trichocarpa x P. deltoides) NADPH-cytochrome  
P450 oxydoreductase isoform 1 mRNA, complete cds.  
ACCESSION AF302496  
VERSION AF302496.1  
KEYWORDS GI:13183561  
SOURCE  
ORGANISM  
Populus x generosa.  
Populus x generosa  
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
Malpighiales; Salicaceae; Populus.  
REFERENCE 1 (bases 1 to 2498)  
AUTHORS Ro, D.-K. and Douglas, C.  
TITLE Functional characterization of cytochrome P450 reductase from the  
hybrid poplar (Populus trichocarpa x P. deltoides)  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 2498)  
TITLE Direct Submission  
AUTHORS Ro, D.-K. and Douglas, C.  
JOURNAL Submitted (05-SEP-2000) Botany, University of British Columbia,  
6270 University Blvd., Vancouver, British Columbia V6T 1Z4, Canada  
FEATURES  
Location/Qualifiers  
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## RESULT 5

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LOCUS ATATRI1 2199 bp mRNA PLN 01-JUN-1992
DEFINITION A.thaliana ATRI1 mRNA for NADPH-cytochrome P450 reductase.
ACCESSION X66016
VERSION X66016.1 GI:16186
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SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 2199)
AUTHORS Pompon, D.M.
TITLE Direct Submission
JOURNAL Submitted (11-MAY-1992) D.M. Pompon, Centre de Genetique Mol du
CNRS, Avenue de la Terrasse, 91198 Gif-Sur-Yvette Cedex, FRANCE
REFERENCE 2 (bases 1 to 2199)
AUTHORS Mignote-Vieux, C.; Kazmaier, M.; Lacroute, F. and Pompon, D.M.
JOURNAL Unpublished
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## RESULT 6

LOCUS A75959 2114 bp DNA PAT 19-OCT-1999  
DEFINITION Sequence 1 from Patent WO9321326.  
ACCESSION A75959  
VERSION A75959.1 GI:6088149  
KEYWORDS

SOURCE

thale cress.

## ORGANISM

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 2114)  
Kazmaier,M. and Lacroute,F.

## AUTHORS

METHOD OF CLONING A DNA SEQUENCE CODING FOR A PLANT

NADPH-CYTOCHROME P450 REDUCTASE AND ASSOCIATED DNA SEQUENCES

Patent: WO 9321326-A 1 28-OCT-1993;

## JOURNAL

ORSAN (FR); KAZMAIER MICHAEL (FR)

## FEATURES

Location/Qualifiers

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Qy	2035	gatgcaagggaaatggccagagatgtccatgcacgttgcataccatctgcccaagaacag	2094						
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RESULT	8
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DEFINITION	Hybrid poplar (Populus trichocarpa x P. deltoides) NADPH-cytochrome P450 oxidoreductase isoform 2 mRNA, complete cds.
ACCESSION	AF302497
VERSION	AF302497.1 GI:13183563
KEYWORDS	Populus x generosa.
SOURCE	Populus x generosa.
ORGANISM	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE	1 (bases 1 to 2493)
AUTHORS	Ro.D.-K. and Douglas,C.
TITLE	Functional characterization of cytochrome P450 reductase from the hybrid poplar (Populus trichocarpa x P. deltoides)
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 2493)
AUTHORS	Ro.D.-K. and Douglas,C.
TITLE	Direct Submission
JOURNAL	Submitted (05-SEP-2000) Botany, University of British Columbia, 6270 University Blvd., Vancouver, British Columbia V6T 1Z4, Canada
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ORIGIN	

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ACCESSION	Z49767		
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KEYWORDS	CPR1 gene; NADPH-cytochrome P450 reductase.		
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AUTHORS	Tranbarger, T. J. and Misra, S.		
TITLE	The molecular characterization of a set of cDNAs differentially expressed during Douglas-fir germination and early seedling development		
JOURNAL	Physiol. Plantarum 95, 456-464 (1995)		
REFERENCE	2 (bases 1 to 2631)		
AUTHORS	Tranbarger, T. J., Forward, B. S. and Misra, S.		
TITLE	Regulation of NADPH-cytochrome P450 reductase expressed during Douglas-fir germination and seedling development		
JOURNAL	Plant molecular biology. 44 (2), 141-153 (2000)		
MEDLINE	21003320		
PUBMED	11117258		
REFERENCE	3 (bases 1 to 2631)		
AUTHORS	Misra, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-MAY-1995) Santosh Misra, Biochemistry and Microbiology, University of Victoria, P.O. Box 3055 Petch Building, Ring Road, Victoria, British Columbia, V8W 3P6, Canada		
REMARK	Revised by [3]		
REFERENCE	4 (bases 1 to 2631)		
AUTHORS	Tranbarger, T.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-AUG-1999) Tranbarger T., Biochemistry and Microbiology, University of Victoria, P.O. Box 3055 Petch Building, Ring Road, Victoria, British Columbia, V8W 3P6, Canada		
REMARK	Revised by [5]		
REFERENCE	5 (bases 1 to 2631)		
AUTHORS	Tranbarger, T.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-MAR-2000) Tranbarger T., Biochemistry and Microbiology, University of Victoria, P.O. Box 3055 Petch Building, Ring Road, Victoria, British Columbia, V8W 3P6, CANADA		
COMMENT	On Mar 23, 2000 this sequence version replaced gi:6523405.		
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Db |||||ACTCGAAGACGGAAAGCTTTGTGAAGAGTCTGCAAAATGAATGGCAGGTATCTACGTGATG 2248  
Qy tctggtgagtcgaatgt 2183  
Db |||||TATGTAATTAATCGT 2264

RESULT 11

AF325101  
LOCUS AF325101 2136 bp mRNA PLN 11-MAR-2001  
DEFINITION Arabidopsis thaliana NADPH-ferrihemoprotein reductase (ATR2)  
(F9N11.60) mRNA, complete cds.  
ACCESSION AF325101  
VERSION AF325101.1 GI:13272460  
KEYWORDS FLI\_CDNA.  
SOURCE thale cress.

ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
Brassicales; Brassicaceae; Arabidopsids.  
REFERENCE 1 (bases 1 to 2136)  
AUTHORS Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M.,  
Palm,C.J., Theologis,A., Ecker,J. and Davis,R.W.  
TITLE Direct Submission  
JOURNAL Submitted (30-NOV-2000) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA  
FEATURES  
source Location/Qualifiers  
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BASE COUNT 595 a 424 c 519 g 598 t  
ORIGIN  
Query Match 33.8%; Score 895.4; DB 8; Length 2136;  
Best Local Similarity 67.3%; Pred. No. 7.6e-193;  
Matches 1335; Conservative 0; Mismatches 626; Indels 24; Gaps 4;

Qy 206 tcattatggtcacaaactagcttcaatgctgattggtgattggttcttcgcattatga 265  
Db |||||TGATTGTTTACCACATCCATTCCTTCTTATTTGGTGGCATCGTTATGCTCGTTTGGAGGA 220  
Qy 266 aatcttgcctcttcaatacaaaacctattgaactataaaaccaataatgataaagaag 325  
Db |||||GATCCGGTTCCTGGGAATTCAAAACGCTGTCGACCTCTTTAGCCCTTTGGTTATTAGCCCTC 280  
Qy 326 aaggggagattgaagttgatctcctggtaaaataaagctcaactatatttttggtaactcaga 385  
Db |||||CTGAGGA---AGAGATTGATGATGGCGCTTAAGAAAGTTTACCATTCTTTTCGGGTACACAAA 337  
Qy 386 ctggtactgctgaaggatttctgaagcattggcagagaataaagcaaaagtaagacaaga 445  
Db |||||CTGGTACTGCTGAAGGTTTTCGAAGGCTTTAGGAGAGAAGAGCTAAAGCAAGATATGAAA 397  
Qy 446 aagcagttgttaagtagttgacctggatgactatgcagccgagagatgatacaataagaag 505  
Db |||||AGACCAGATTCAAAATCGTTGATTTGGATGATTACCGCGCTGATGATGATGATGATGAGG 457  
Qy 506 agaaattaaagaagagcttcttgggttttctcagtggttagccacttatggtgatggtgagc 565  
Db |||||AGAAATTCAGAAAGAGGATGTTGGCTTCTTCTTCTTACCCACATATGAGATGTTGAGC 517  
Qy 566 caactgacaatgctgcgagattttacaaatggttcaactcaggaacatgaaaggggagagc 625  
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MQERLAKESGAEELGSVALVPGCRNRLDFIYEDELNHFVETGAISMEVYAFREGRPA  
KEYVOHRMSKSEIMDMISHGAIYVCGDAKGWARDVHRMLHTIAEQGALDSSHAE  
SLVKNHMSGRYLRDWM"  
BASE COUNT 709 a 454 c 644 g 749 t  
ORIGIN

Query Match 33.0%; Score 875.2; DB 8; Length 2556;  
Best Local Similarity 67.9%; Pred. No. 2.9e-188;  
Matches 1276; Conservative 0; Mismatches 583; Indels 21; Gaps 3;

Qy	319	aaagaagaagaggagattgaattgatcctggttaaaattaaagctcaactatatatttttgtt	378
Db	275	AAATTTGAAATGGAGGAGGAAGTTGATGACGGTAAAAAGAGGTTACGATTTTTACGGT	334
Qy	379	actcagactggtactgctgaaggatttqtaagcattgagcagagaataaagcgaag	438
Db	335	ACTCAGACCGGTACTGCTGAAGGTTTGTCTAAGGCACCTTGGGAGGAGGCCGAAGCAGA	394
Qy	439	tacaagaacagctgtttaagtagtgtagctgtagtactgtagcagcagagtagatcaaa	498
Db	395	TATCAGGATGCTACTTTTAAACATTATTGATTTGGATGATTATGCGGGTGATGACGAG	454
Qy	499	tatgaagaagaataaagaagaagctcttgggtgttttttcaatggtagcacttatggtagt	558
Db	455	TATGACAGCAAACTTAAAGAAAGATCTATGGTGTCTTCTTTAGCCACCATATGGTGAT	514
Qy	559	ggtgagcaactgcaatgctgcgagattttacaatggttccactcaggaacatgaag	618
Db	515	GGTGNACCCACCGACATGACGACGAGATTTTACAAGTGGTTTTGTGAGGGCAAGAGAGA	574
Qy	619	ggagatgggtcttcagcaactaacttatgggtgtttttgggttaaccgtcaatcacgag	678
Db	575	GGGAGTGGCTTAACAATCTTCAATATGGTGTGTTGGCTTGGCAACAGGCAATATGAG	634
Qy	679	catittcaacaagatcgcggtagatgtgtagtagcaactcggtaacaaggtgcgaagcgc	738
Db	635	CATTTCACAAGATGTCAGTGGTGTGGATGACGGCCCTTTGTGACGAGGGTGCCAAGCGT	694
Qy	739	attgttcaagtgggctcggtgacgatgaatgcattgaagatgattttactgtctgg	798
Db	695	CTTGTTCAGTGTGATGGGAGATGACGACCAATGTATTGAAGATGACTTTTACTGCATGG	754
Qy	799	cgagaattgtgtgactgaatttgatcagttgtctcaagaatgagggatgctgctccctca	858
Db	755	CGGAGTTAGTCTGGCTGAGTGGATCAACTGCTCTTGGACGAGGAGCTCTAAGGCTGCT	814
Qy	859	gtggctaacacgatatattgttactgttctctgaatacacagggtagtgattcaag---	915
Db	815	---GCAACTCCATACAGCTGCTGTGTAGAAATATCGTTGATGCTTTTAAATCAAACT	871
Qy	916	acggtcgcgctctggatgataaacacataaactcgtctaacgcgcatgttgcatattgat	975
Db	872	GATACATCATCTCCACTGGTTTCGGAGTATGAGCAAAATTAATGGCCATGCTGTATATGAT	931
Qy	976	attctccatctcttggaacacatttgttgcctcaaaagaagagagctcccaaaacccaagtct	1035
Db	932	GCTCAACATCCCTCGAGGGCTTAATGTGGCTCTTAAGAAGAGAGCTTCATACACCTGCATCG	991
Qy	1036	gatagatcctgtatcacatctcgtgaggttcgaacatacaaggctcttcccttaacatagagact	1095
Db	992	GATGTTCTCTGACCCCATCTGGAGTTCGATATTTCTCTACTGACCTTGCATATGAAACT	1051









Qy	746	aagtggggctcggugacgatgaatgcattgaagaagtatttactgtcttgccggagaat	805
Db	828	AAGTTGGTCTTGAGATGATGACCACTGTATTTCAGATGCACCTTTACCGCTTGGCAGAAG	887
Qy	806	tgttgtgacctgaattcgatcagttgctcaaaagatgaagatgctgctcttcctcagtgcta	865
Db	888	CATTGTGCCCGGAGCTTGATACAATACTCAGGGGAAGAAGGGATACACGCT---GTTGCCA	944
Qy	866	caccgtatatgtactgttctcctgaatacacaggtagtgatitcacgaacaactacgctcgcg	925
Db	945	CACCATACACTGCAGCTGTGTTTAGAATACAGAGTTTCTATTCCACGACTCTCGAAATGCCA	1004
Qy	926	ctctggatgataaacacataataactgctaaocggcgaigtgtgcatttggatatcttcccact	985
Db	1005	AATTCAATGATATAACATTGGCAATGGCAATGGTTACACTGTGTTTGTATGCTCAACATC	1064
Qy	986	cttgagaaacccattgttgtctcaacaaaagagadctccaaacccaagctcgtatagatctct	1045
Db	1065	CTTACAAGCAAAATGTCGTGTATAAAGGGAGCTTTCATACTCCCAGTCTCATCGTCTCTT	1124
Qy	1046	gtatacatctggagttcgacatatcaggtctctcccttacatatgagagctgagagatcatg	1105
Db	1125	GTATCCATTTTGGTAATTGACATTGCTGGAAAGTGGACTTTACGATGNAACTTGGAGATCATG	1184
Qy	1106	ttgggtgttatgctgagaactcgatgaaactgtcgagaagcagggaagcgtgttggtgc	1165
Db	1185	TGGTGTACTTCTGTGATAACTTAAAGTGAACCTGTAGATGAAGCTCTTAGATTGCTGGATA	1244
Qy	1166	aacccttggaattgtgtgttttcaaattccacaggaataaagaagacgggtcaeccaccaggaa	1225
Db	1245	TGTCACCTGATACATTATTTCTCACCTTCAGCTGFAAAAAGAGAGCGGCACCAATCAGCA	1304
Qy	1226	gctcattaccacactctcttcccaggctccttgcaaccttaagcatctgcctcagcagcctatg	1285
Db	1305	GCTCACTGCCTCTCCCTTCCCCA--CCTTGCACACTTGAGAACACGGCTTACAGATATG	1361
Qy	1286	ctgatcttttgaatcctcctagaaagcttctctgatgtctctgtcgcgtcatgcatctg	1345
Db	1362	CATGCTCTTTTGTAGTTCTCCAAGAAGATCTGCTTTAGTTTGGCTTGGCTGCTCATGCATCTG	1421
Qy	1346	taccagtagaagcagagaagatgcgcttttctcatacctctcgggaagaataagattt	1405
Db	1422	ATCTACCGAAGCAGAACGATTAANAACACTTGCCTTTCACCTGCTGGAAGAAGATGAATATT	1481
Qy	1406	caaaatgggtagttggaagtcagagagtgcttttggagatcatggccgagtttccatcag	1465
Db	1482	CAAAGTGGGTAGTAGAGCTCAAGAAGTCTACTTGGAGTGTGATGGCCGAGTTCCTTTTCAG	1541
Qy	1466	caaaaceccccctcttgggtgttcttcttgctgaagtagccctctogcttaccgctcgtact	1525
Db	1542	CCAAGCCACCACATTTGTTGTCTTTCGCTFGSAGTTGCTTCCAAGGTTTGCAGCGCTAGGTCT	1601
Qy	1526	attctatctcatcctctctaagtttgcctccctcaagaatticattgtagcgtgtcctttag	1585
Db	1602	ATTGATATCATCATGCCCAAGATTGCTTGAACCTAGAAATTCACGCTCATGTGCATCTGG	1661
Qy	1586	tatatgtcaaaagccctacggaaggtttcaoccgaggagtggttctcgacatggatgaagc	1645
Db	1662	TTTTATGAAAAATGCCAACTGGCAGGATTTCATAAGGGAGTGTGTTCCACTTGGATGAAGA	1721
Qy	1646	atgcagttctctcaggata-----gctgggctcctctatttttgtctcgaa	1687
Db	1722	ATGCTGTGCTTACAGAGAAGAGTGAANAACTGTTCTCTCGGGCGCCGATATTTCGTTAGCG	1781
Qy	1688	cgtaaaacttcaaagtlaccagctgcacccctcaactccaatlatactggtggacctcgta	1747
Db	1782	ANTCCAACCTTCAAGCTTCTCTGTGATTCTAAGGTACCAGTCATCATGATCGGTCACGGGA	1841
Qy	1748	cagggttagctctcttcagagatttctgcaggaagaagatggccctcaaggaaaaatggtg	1807
Db	1842	CTGGATTAGCTCATTCAGAGATTTCTTTCAGGAAGAAGACTAGCGTTGGTACGAATCTGGT	1901

QY	1808	ctcaacttggcccgagcgtgctcttttcgcgatgtaggaaatcgtaatatggaacttcattt	1867
Db	1902	TTGAACCTTTGGGCGCATACGTTTTGTCTTTTGATGCAGAAACCGTAGAATTGATTCATCT	1961
QY	1868	atgaagacgaactaaacaacttcgttggaacgagagtgcatcttcgagagtagttattgcct	1927
Db	1962	ACGAGGAAGAGCTCCAGCGATTTGTTGAGAGTGGTCTCCTCGCAGAGTAAGTGTCTGCGCT	2021
QY	1928	tttcacgtggaaggggaaaaagaaggaatagtttcaacataaagatgatgagaaaacaacgg	1987
Db	2022	TCTCTCTGAGAGGCCACCACCAAGAATAACGTACACCACAAGATGATGCAAGGCTTCTG	2081
QY	1988	atgtatggaatgtgatcatcaggggacggttatctctctatgttgttgtaatgccaaaggaa	2047
Db	2082	ATATCTGCAATATGATCTCTCAAGGAGCTTATTTATATATGTTTGGTGACGCCAAAAGSCA	2141
QY	2048	tggccagagatgtccatgcgcagtgtgcataccattgcccaagaacagggaccatggaat	2107
Db	2142	TGGCAAGAGATGTTCCACAGATCTCTCCACACAATAGCTCAAGAACACAGGGGTCAATGGATT	2201
QY	2108	cattctgtccgaagctgcagtaaagaacacctcaagttgaaagaacgatatactaagagatg	2167
Db	2202	CAACTAAAGCAGAGGGCTTCGTGAAGAATCTGCAAACGAGTGAAGATATCTTAGAGATG	2261
QY	2168	tctggatgacgaa	2180
Db	2262	TATGGTAACGAA	2274
RESULT	15		
AF024634			
LOCUS	AF024634	2466 bp mRNA PLN 26-JAN-1998	
DEFINITION	Petroselinum crispum NADPH cytochrome P450 reductase (CPR2) mRNA,		
	complete cds.		
ACCESSION	AF024634		
VERSION	AF024634.1	GI:2809384	
KEYWORDS	.		
SOURCE	parsley.		
ORGANISM	Petroselinum crispum		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.		
REFERENCE	1 (bases 1 to 2466)		
AUTHORS	Koopmann,E. and Hahlbrock,K.		
TITLE	Differentially regulated NADPH:cytochrome P450 oxidoreductases in		
JOURNAL	parsley		
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 94 (26), 14954-14959 (1997)		
REFERENCE	98070859		
AUTHORS	2 (bases 1 to 2466)		
TITLE	Koopmann,E. and Hahlbrock,K.		
JOURNAL	Direct Submission		
FEATURES	Submitted (12-SEP-1997) Biochemistry, Max-Planck-Institut fuer		
source	Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln 50829, Germany		
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BASE COUNT 660 a 474 c 617 g 715 t  
ORIGIN

Query Match 33.08; Score 874; DB 8; Length 2466;  
Best Local Similarity 66.38; Pred. No. 5.5e-188;  
Matches 1296; Conservative 0; Mismatches 640; Indels 18; Gaps 2;

Qy	286	aaacattatgaacattataaaccataattgataaagaagaagagagattgaagtgtat	345
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Qy	346	cctggtaaaataaagctcacatatatttttggtaactagactggtaactgctgaaggattt	405
Db	280	GACGGTAAAAAGAAAGTTACCGTGTTTTTCGGCACTCAAACTGGTACTGCTGAAGGCTTT	339
Qy	406	gctaaggcattggcagaagaataaaggcaaaagtacaagaagaagcagttggttaaagtatt	465
Db	340	GCTAAGGCTTTTTCGGGAGGAGCGGAAAGCGCGGTACGAGAAGCGGAAATTGAGAGTTGTT	399
Qy	466	gacctggatgactatgcagccgagagatgatacaatgaagagaataaagaagaagctct	525
Db	400	GATTAGATGATTATGCGCGGAGGATGAGGAGTACGAGGCGCAAAATTTAAGAACGAATCT	459
Qy	526	ttgggttttttcattgtagccacttattggtgatgtagcgcacactgacaatgctgcgaga	585
Db	460	TTTGGCTTTTCTCTTACGTACATATGCTGACGGTGAGCCAACTGACAATGCGGCTAGA	519
Qy	586	ttttacaaatggttcactcagaagaacataaaggggagagtggtcttcacgaactaacttat	645
Db	520	TTCTATAAGTTGGTTTTCGGAGGGTGAAGAGAAAGAGATTTGTTAAATTAAGCTTCAAT	579
Qy	646	ggtgttttttgggttggttaacgtcaatcacgagcatttcaacaagatcgcgtagatgtg	705
Db	580	GGAGTGTGTGGCTTTGGAATAGGCAGTACGAAACATTTTAAACAGATCGCAAAAGTTGTT	639
Qy	706	gatgaacactcgtgtaaacagggtgcgaagcagcattgttcgaagtggtgctgcgtgacgat	765
Db	640	GACCATGCTCTGTCAGATCAGGGAGCCAAAGCGTATTGTTGAAGTGGGTATGGTGATGAT	699
Qy	766	gatcaatgcatgaagatgattttactacttggcgagaaattgtgtgactgaattgcat	825
Db	700	GATCAATGCATTGAAGATGACTTACCCCATGGCGGGAAATGGTCTGGCCCTGAATTGGAT	759
Qy	826	cagttgtcaaagatgaggatgctgctcttcagtggtacacacgtatatgtgctactgtt	885
Db	760	AAGTTGCTTTTGGATGAGGA--TGACACATCTGCTGCAACTCCTTTACACAGCTGCTGTT	816
Qy	886	cctgaatacagggtagtgattcaogaaactacggtcgcggtctcggatgataaacaacata	945
Db	817	TTGGAATATCGGGTGTGGTTTATGACCAACTTGTATACAGCTTACAGCTGATCGGAGTTTA	876
Qy	946	aatactgctaagcgcatgtgtcatttgatatattccatccttgcagaaacattgttct	1005
Db	877	AGTACCCAAAATGGCGATACAGTTTCATGCTCAACATCCGTGCGAGGCTTAGCGCTAGCT	936
Qy	1006	caacaagaagagctccacaacccaagctctgatagatcctgtatatacatctgaggtcgac	1065
Db	937	GCAAGAAAGAGCTTCAATAACCTGCATCTGATCTGCTGCTGCATTCACTTGGAGTTTGAC	996
Qy	1066	atacaggtctcttccttacataagactggagatcatgtttggtgttttatgctgagAAC	1125
Db	997	ATTTCCACACACGGGCTTGCATATGAACACTGGTGACCACGTCGGGGTCTACTGTGAGAAT	1056
Qy	1126	tgcatgaacactgtcgagaagcagggaagcagcagcagcagcagcagcagcagcagcagc	1185
Db	1057	CTGGTTGAATTTGTTGAGGAGGCTGAAAAGCTATTAGGCATGCAACCAACCACTTACTTTC	1116

Qy	1186	tcaattcacaggataaaagaagaagcgggtcaccgccagggaagctcattaccacacctcttc	1245
Db	1117	TCTGTCCATATTGACGACGAAGATGSAACACACACTTACTGGAGGCTCTCTGCCACCTCCC	1176
Qy	1246	ccaggtccttcacaccttaagcatctgcccctagcacgctatgctgatatcttttgaaacctct	1305
Db	1177	TTCCGCCCATGCACGTGTGAGAAGTGCACGTGGCAAAATATGCAGATCTTTTGTAGCTCTCG	1236
Qy	1306	agaaggcttctctgattgctctgcccctcatctgtaccctcagtgaaacagagaga	1365
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Qy	1662	-----tagctgggtcctctattttgtcgaagtcgaactcaagctcaagctcagcgt	1710
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Qy	1711	gacctcctcaactcccaatttatcatggtgggacctgtgtcagggcttagctccttccagaga	1770
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Qy	1771	ttctgcaggaagaagaatggccctcaaggaataatggtgtcctcaacttggccccagcagtctc	1830
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Qy	1831	ttttcggatgtaggaatcgtaatatggaactcattatgaagacgaactaaacaacttc	1890
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Db	1837	GTGAAAGTGGTTCAATCTCTGAGCTAAATTTGTAGCTTTCTCACGTGAGGGGCCACTAAG	1896
Qy	1951	gaatgttcaacataatgatgagagaagaacacggaatgatatgaaatgtgatatacagg	2010
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Qy	2011	gacggttatctctatgtgtgtgtggtcgaatcgaagggaatggccagagatgtccatcgacg	2070
Db	1957	GGTGATATATTTATGTCTGCGGTGATGCAAAAGCATGGCCAGGATGCCATCGCATG	2016
Qy	2071	ttgtacacatttggcccaagaacaggagaccatlggaatcatctgtgctgcgaagctgcagta	2130
Db	2017	CTTCACAAATTCACAGGAGCAGGAGCTCTTGACACGACGAGCGAGAGCTGGGTT	2076
Qy	2131	aagaacacctcaagtttgaagaacgaatatcgaagagatgtctggtgatcgaatgtagcttgc	2190
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Qy	2191	caagtcctcccttttctggctggtctgtttatggt	2224
Db	2137	AGCCGACCTTGGTTATGTAGATAAGTTTATGAT	2170

Search completed: December 27, 2001, 14:12:13  
Job time: 6223 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 12:28:30 ; Search time 224.31 Seconds  
(without alignments)  
10124.625 Million cell updates/sec

Title: US-09-486-757-10  
Perfect score: 2649  
Sequence: 1 cggcagcagctgttagtat.....ttttgagaaaaa 2649

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	2645.8	99.9	2650	AA08517	Poppy cytochrome P
2	983.4	37.1	2114	AA051236	Plant NADPH cytoch
3	958.6	36.2	2558	AA08520	Poppy cytochrome P
4	895.4	33.8	2136	AA044709	Arabidopsis thalia
5	875	33.0	2423	AA051237	Plant NADPH cytoch
6	859.8	32.5	2112	AA051238	Plant NADPH cytoch
7	231.8	8.8	485	AA035800	Zea mays DNA fragm
8	192.8	7.3	1872	AA065716	Oxidoreductase gen
9	192.8	7.3	3435	AA081743	Plasmid pAMP19.
10	192.8	7.3	3453	AA081746	Plasmid pALP25.
11	191.4	7.2	3399	AA081747	Plasmid pALP4. A

12	191.2	7.2	2037	8	AA070925	Sequence encoding
13	191.2	7.2	3453	9	AA081744	Plasmid pALP1. A
14	187.6	7.1	2450	8	AA070605	Plasmid pRF1 encod
15	170.4	6.4	3489	9	AA081745	Plasmid pALP17.
16	169.4	6.4	3310	21	AA029331	Partial sequence o
17	169.4	6.4	3311	21	AA0293079	Partial sequence o
18	167.4	6.3	8475	22	AA076964	Genetic construct
19	167.4	6.3	8492	22	AA076963	Genetic construct
20	167.4	6.3	8537	22	AA076962	Genetic construct
21	167.2	6.3	1872	9	AA081748	Plasmid pAXP2. A
22	165.4	6.2	2034	22	AA076960	Human derived cyto
23	165.4	6.2	2034	22	AA076961	Human derived cyto
24	162.4	6.1	2403	20	AA0219778	Human P450 reducta
25	162.4	6.1	2403	20	AA0207749	Human P450 reducta
26	159	6.0	1851	20	AA0219779	Human anchorless P
27	159	6.0	1851	20	AA0207750	Human P450 reducta
28	155.6	5.9	2049	22	AA026033	DNA encoding rabbl
29	114	4.3	936	22	AA058252	Oligonucleotide D1
30	114	4.3	936	22	AA058254	Oligonucleotide D1
31	114	4.3	936	22	AA058257	Oligonucleotide D1
32	114	4.3	936	22	AA058259	Oligonucleotide D2
33	114	4.3	936	22	AA058262	Oligonucleotide D2
34	114	4.3	938	22	AA058255	Oligonucleotide D1
35	112.6	4.3	936	22	AA058252	Oligonucleotide D1
36	112.6	4.3	936	22	AA058254	Oligonucleotide D1
37	112.6	4.3	936	22	AA058257	Oligonucleotide D1
38	112.6	4.3	936	22	AA058259	Oligonucleotide D1
39	112.6	4.3	936	22	AA058262	Oligonucleotide D2
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41	111.8	4.2	4145	21	AAA30567	Oligonucleotide D1
42	108	4.1	4206	21	AAA30566	Genomic DNA encodi
43	102.8	3.9	3155	22	AA054060	S. epidermidis gen
44	102.8	3.9	4055	22	AA053993	S. epidermidis gen
45	99.6	3.8	4151	20	AA023663	B. bassiana POPs r

#### ALIGNMENTS

RESULT 1  
AA08517  
ID AA08517 standard; DNA; 2650 BP.  
XX  
AC AA08517;  
XX  
DT 19-JUL-1999 (first entry)  
XX  
DE Poppy cytochrome P450 reductase.  
XX  
KW Opium poppy; alkaloids; cytochrome P450 reductase; morphine;  
KW codeine; oripavine; thebaine; transformation; crop yield; probe;  
KW primer; ss.  
XX  
OS Papaver somniferum.  
XX  
FH Key Location/Qualifiers  
CDS 124..2175  
FT /\*tag=a  
FT /product= "Cytochrome P450 reductase"  
XX  
PN W09911765-A1.  
XX  
PD 11-MAR-1999.  
XX  
PF 28-AUG-1998; 98WO-AU00705.  
XX  
PR 29-AUG-1997; 97AU-0008872.  
XX  
PA (JOHJ) JOHNSON & JOHNSON RES PTY LTD.  
XX  
PI Atkins DG, Fist AJ, Kutchan TM, Zenk MH;  
XX  
DR WPI; 1999-214703/18.

DR P-PSDB: AAW85680, AAW85682.

PT Nucleic acid encoding cytochrome P-450 reductase from poppy

XX  
PS  
Claim 3: Fig 9a: 58pp: English.

Transforming plants with a nucleic acid molecule encoding cytochrome P450 reductase alters the yield and/or type of alkaloids produced. In opium poppies it specifically increases the yield of medically useful alkaloids such as morphine, codeine, oripavine and thebaine. Sequences complementary to the coding sequence of cytochrome P450 reductase are useful as probes, primers and antisense sequences, or for design of ribozymes, transformation with DNA encoding the cytochrome P450 reductase allows regulation of the total alkaloid content and of the relative proportions of individual alkaloids. Content of the relative proportions of individual alkaloids produced. Increasing the alkaloid content of poppy straw should reduce the cost of alkaloid production. Cytochrome P450 reductase is the rate-limiting enzyme in biosynthesis of alkaloids in poppies. Peptide fragments of the cytochrome P450 reductase are described in AAW85673-W85678.

Sequence 2650 BP; 766 A; 514 C; 606 G; 764 T; 0 other;

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Query Match      99.9%; Score 2645.8; DB 20; Length 2650;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2647; Conservative 0; Mismatches 2; Indels 0;
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Qy	121	attatgggttcgaataaatttagctaatctogattgaatcgcgatgttaggaatacaatagga	180
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AC					
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XX					
DT 11-MAY-1994 (first entry)					
XX					
DE Plant NADPH cytochrome P450 reductase (ara B).					
XX					







[illegible]

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AC				
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DT				
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KW	Hybridisation assay; genetic mapping; gene expression control;			
KW	protein identification; signal transduction pathway;			
KW	metabolic pathway; promoter; termination sequence; ss.			
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OS	Arabidopsis thaliana.			
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PF	25-FEB-2000; 2000EP-0301439.			
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PR	25-FEB-1999; 99US-0121825.			
PR	05-MAR-1999; 99US-0123180.			
PR	09-MAR-1999; 99US-0123548.			
PR	23-MAR-1999; 99US-0125788.			
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 Db 815 caccatacactgctgctgtgtagaatacagagtttctattcacgactctgaagatgcca 874  
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 Db 875 aattcaatgataaaacatggcaaatgggaatggttacactgtgttgatgctcaacatc 934  
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 QY 1931 cactggaaggggaaagaaggaatgtttcaacataaagatgatgagaagaacacgagatg 1990  
 Db 1892 ctctggaagggcccccacaaagaatcgtacacaaagatgatggacaaggtctctgata 1951  
 QY 1991 tatgaaatgtgatatcaggggacgttatctctatctgtgtgtgtgatgccagggaatgg 2050  
 Db 1952 tctggaatatgactctcaaggagcttatttatagtttgtgtgacgccaaagcatgg 2011  
 QY 2051 ccagagatgctcatcgcagcttgcatcacattgcccagaacacaggggacccatggaaatc 2110  
 Db 2012 caagagatgttcacagatctctccacaaatagctcaagaacaggggtcaatggattcaa 2071  
 QY 2111 ctgctgcggaagctgcagttaaagaacactccaagttgaagaacgatatctaaagagatgct 2170  
 Db 2072 ctaaagcagaggggttcgtgaaagaactctgcaaacagagtggaaagatatcttagagatct 2131  
 QY 2171 ggtga 2175  
 Db 2132 ggtaa 2136

RESULT 5  
 AAQ51237  
 ID AAQ51237 standard; cDNA: 2423 BP.  
 XX  
 AC AAQ51237;  
 XX  
 DT 11-MAY-1994 (first entry)  
 XX  
 DE Plant NADPH cytochrome P450 reductase (ara C).  
 XX  
 KW NADPH cytochrome P450 reductase; functional complementation;  
 XX identification; ss.  
 OS Arabidopsis thaliana.  
 XX

PH key Location/Qualifiers  
 FT CDS  
 FT 131..2269  
 FT /\*tag= a  
 FT /product= NADPH cytochrome P450 reductase.  
 FT misc\_difference 374..376  
 FT /\*tag= b  
 FT /transl\_except= CGT encodes Lys.  
 FT misc\_difference 410..412  
 FT /\*tag= c  
 FT /transl\_except= CGT encodes Lys.  
 FT misc\_difference 434..436  
 FT /\*tag= d  
 FT /transl\_except= CGT encodes Lys.  
 FT misc\_difference 518..520  
 FT /\*tag= e  
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 FT /\*tag= f  
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 FT misc\_difference 1091..1093  
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 FT misc\_difference 1946..1948  
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 FT misc\_difference 2255..2257  
 FT /\*tag= ai  
 FT /transl\_except= AGA encodes Lys.  
 FT WO9321326-A.  
 FT 28-OCT-1993.  
 FT 13-APR-1993; 93WO-FR00367.  
 FT 13-APR-1992; 92FR-0004491.  
 FT (ORSA-) ORSAN.  
 FT Kazmaier M, Lacroute F, Mignotte-vieux C, Minet M;  
 FT Pompon D;  
 FT WPI; 1993-351736/44.  
 FT P-PSDB; AAR43582.  
 FT New DNA encoding plant NADPH cytochrome P450 reductase - cloned  
 FT by functional complementation in yeast, also recombinant enzyme  
 FT useful in P450 mediated bioconversion processes  
 FT Claim 11; Figure 10; 79pp; French.  
 FT A new method for determining whether a DNA sequence encodes an NADPH  
 FT cytochrome P450 reductase involves transforming yeasts with plasmids  
 FT of a total cDNA bank of plant(s). The yeasts used in the procedure  
 FT are incapable of producing their own NADPH cytochrome P450  
 FT reductase. They are then exposed to a cytochrome P450 inhibitor at a  
 FT level which is lethal to the yeast cells but not to cells which,  
 FT because of the transformation, now contain an active NADPH  
 FT cytochrome P450 reductase. Surviving clones are then isolated and  
 FT plasmid DNA extracted. The gene is inserted into the plasmid at a  
 FT site which places it under the control of an inducible promoter.  
 FT SQ Sequence 2423 BP; 674 A; 497 C; 552 G; 700 T; 0 other;

Query Match 33.0%; Score 875; DB 14; Length 2423;  
 Best Local Similarity 66.5%; Pred. No. 4.5e-225;  
 Matches 1326; Conservative 0; Mismatches 640; Indels 27; Gaps 4;





QY 626 ggttcagacaactaatgtgtttttgtttgttggttaacctcaatacagaatttca 685  
 Db 461 ggtctgaaacactcaactatggtgtttttgtttgttggttaacctcaatacagaatttca 520  
 QY 686 acaagatcggttagatgttggttagagcaactcgtgaaacaaggtgcaaaagcattgttc 745  
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 QY 746 aagtggtgctggtgacgatgatcaatgaatgaatgaatgaatgaatgaatgaatgaat 805  
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 QY 2111 ctgctgcggaagctgcagtaaaagaactccaagttgaaagaacgatatctaaagatgtct 2170  
 Db 1952 ctaaagcagagctgtatgtggaagatctacaataatgctcggaagataacctccgtgatgttt 2011  
 QY 2171 ggtgatga 2179  
 Db 2012 ggtgatcta 2020

RESULT 7  
 AAC35800 ID AAC35800 standard; DNA; 485 BP.  
 XX AC AAC35800;  
 XX DT 17-OCT-2000 (first entry)  
 XX DE Zea mays DNA fragment SEQ ID NO: 11470.  
 KW Hybridisation assay; genetic mapping; gene expression control;  
 KW protein identification; signal transduction pathway; metabolic;  
 KW pathway; promoter; termination sequence; corn; ss.  
 XX OS Zea mays subsp. mays.  
 XX PN EP1033405-A2.  
 XX PD 06-SEP-2000.  
 XX PF 25-FEB-2000; 2000EP-0301439.  
 XX PR 25-FEB-1999; 99US-0121825.  
 PR 05-MAR-1999; 99US-0123180.  
 PR 09-MAR-1999; 99US-0123548.  
 PR 23-MAR-1999; 99US-0125788.  
 PR 25-MAR-1999; 99US-0126264.  
 PR 29-MAR-1999; 99US-0126785.  
 PR 01-APR-1999; 99US-0127462.  
 PR 06-APR-1999; 99US-0128234.  
 PR 08-APR-1999; 99US-0128714.  
 PR 16-APR-1999; 99US-0129845.  
 PR 19-APR-1999; 99US-0130077.  
 PR 21-APR-1999; 99US-0130449.  
 PR 23-APR-1999; 99US-0130510.  
 PR 23-APR-1999; 99US-0130891.



PR	28-APR-1999;	990S-0131449.	PR	21-JUL-1999;	990S-0144814.
PR	30-APR-1999;	990S-0132048.	PR	21-JUL-1999;	990S-0145086.
PR	30-APR-1999;	990S-0132407.	PR	21-JUL-1999;	990S-0145088.
PR	04-MAY-1999;	990S-0132484.	PR	22-JUL-1999;	990S-0145085.
PR	05-MAY-1999;	990S-0132485.	PR	22-JUL-1999;	990S-0145087.
PR	06-MAY-1999;	990S-0132486.	PR	22-JUL-1999;	990S-0145089.
PR	06-MAY-1999;	990S-0132487.	PR	22-JUL-1999;	990S-0145192.
PR	07-MAY-1999;	990S-0132863.	PR	23-JUL-1999;	990S-0145145.
PR	11-MAY-1999;	990S-0134256.	PR	23-JUL-1999;	990S-0145218.
PR	14-MAY-1999;	990S-0134218.	PR	23-JUL-1999;	990S-0145224.
PR	14-MAY-1999;	990S-0134219.	PR	26-JUL-1999;	990S-0145276.
PR	14-MAY-1999;	990S-0134221.	PR	27-JUL-1999;	990S-0145913.
PR	14-MAY-1999;	990S-0134370.	PR	27-JUL-1999;	990S-0145918.
PR	18-MAY-1999;	990S-0134768.	PR	27-JUL-1999;	990S-0145919.
PR	19-MAY-1999;	990S-0134941.	PR	28-JUL-1999;	990S-0145951.
PR	20-MAY-1999;	990S-0135124.	PR	02-AUG-1999;	990S-0146386.
PR	21-MAY-1999;	990S-0135353.	PR	02-AUG-1999;	990S-0146388.
PR	24-MAY-1999;	990S-0135629.	PR	02-AUG-1999;	990S-0146389.
PR	25-MAY-1999;	990S-0136021.	PR	03-AUG-1999;	990S-0147038.
PR	27-MAY-1999;	990S-0136392.	PR	04-AUG-1999;	990S-0147204.
PR	28-MAY-1999;	990S-0136782.	PR	04-AUG-1999;	990S-0147302.
PR	01-JUN-1999;	990S-0137222.	PR	05-AUG-1999;	990S-0147192.
PR	03-JUN-1999;	990S-0137528.	PR	05-AUG-1999;	990S-0147260.
PR	04-JUN-1999;	990S-0137502.	PR	06-AUG-1999;	990S-0147303.
PR	07-JUN-1999;	990S-0137724.	PR	06-AUG-1999;	990S-0147416.
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PR	10-JUN-1999;	990S-0138847.	PR	10-AUG-1999;	990S-0148171.
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PR	16-JUN-1999;	990S-0139452.	PR	12-AUG-1999;	990S-0148341.
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PR	18-JUN-1999;	990S-0139460.	PR	23-AUG-1999;	990S-0149902.
PR	18-JUN-1999;	990S-0139461.	PR	23-AUG-1999;	990S-0149930.
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PR	18-JUN-1999;	990S-0139763.	PR	27-AUG-1999;	990S-0151066.
PR	21-JUN-1999;	990S-0139817.	PR	27-AUG-1999;	990S-0151080.
PR	22-JUN-1999;	990S-0139899.	PR	30-AUG-1999;	990S-0151303.
PR	23-JUN-1999;	990S-0140353.	PR	31-AUG-1999;	990S-0151438.
PR	23-JUN-1999;	990S-0140354.	PR	01-SEP-1999;	990S-0151930.
PR	24-JUN-1999;	990S-0140695.	PR	07-SEP-1999;	990S-0152363.
PR	28-JUN-1999;	990S-0140823.	PR	10-SEP-1999;	990S-0153070.
PR	29-JUN-1999;	990S-0140991.	PR	13-SEP-1999;	990S-0153758.
PR	30-JUN-1999;	990S-0141287.	PR	15-SEP-1999;	990S-0154018.
PR	01-JUL-1999;	990S-0141842.	PR	16-SEP-1999;	990S-0154039.
PR	01-JUL-1999;	990S-0142154.	PR	20-SEP-1999;	990S-0154779.
PR	02-JUL-1999;	990S-0142055.	PR	22-SEP-1999;	990S-0155139.
PR	06-JUL-1999;	990S-0142390.	PR	23-SEP-1999;	990S-0155486.
PR	08-JUL-1999;	990S-0142803.	PR	24-SEP-1999;	990S-0155659.
PR	09-JUL-1999;	990S-0142920.	PR	28-SEP-1999;	990S-0156458.
PR	12-JUL-1999;	990S-0142977.	PR	29-SEP-1999;	990S-0156596.
PR	13-JUL-1999;	990S-0143542.	PR	04-OCT-1999;	990S-0157117.
PR	14-JUL-1999;	990S-0143624.	PR	05-OCT-1999;	990S-0157753.
PR	15-JUL-1999;	990S-0144005.	PR	06-OCT-1999;	990S-0157865.
PR	16-JUL-1999;	990S-0144085.	PR	07-OCT-1999;	990S-0158029.
PR	16-JUL-1999;	990S-0144086.	PR	08-OCT-1999;	990S-0158232.
PR	19-JUL-1999;	990S-0144325.	PR	12-OCT-1999;	990S-0158369.
PR	19-JUL-1999;	990S-0144331.	PR	13-OCT-1999;	990S-0159293.
PR	19-JUL-1999;	990S-0144332.	PR	13-OCT-1999;	990S-0159294.
PR	19-JUL-1999;	990S-0144333.	PR	13-OCT-1999;	990S-0159295.
PR	19-JUL-1999;	990S-0144334.	PR	14-OCT-1999;	990S-0159329.
PR	19-JUL-1999;	990S-0144335.	PR	14-OCT-1999;	990S-0159330.
PR	20-JUL-1999;	990S-0144352.	PR	14-OCT-1999;	990S-0159331.
PR	20-JUL-1999;	990S-0144632.	PR	14-OCT-1999;	990S-0159637.
PR	20-JUL-1999;	990S-0144884.	PR	14-OCT-1999;	990S-0159638.



Db 582 ccacgaagacatggaogtagcgaagtggtacacgggtgagatggtggtcctctgaagagcta 641  
Qy 951 tgcatacggcgatgttgcaatttgatattccatctctgcagaacattgtgtgctcaaca 1010  
Db 642 cgagaacagaacccccctctgatgctaagaatccattccctggtctggtccacgcgcaa 701  
Qy 1011 agagagatcccaaaccaacgaatgtagatagatccctgtatatacatctggagttgcagatc 1070  
Db 702 ccggaagctgaaccaaggca---ctgagcggcatctaatgcacctggagttggacatctc 758  
Qy 1071 aggcctctcccttatcatatgaacactggagatcatgttggtgtttatgctgagaaactgga 1130  
Db 759 agactccaagaacaggtatgaactggagatcacgtggtgtgtccacgaccaatgactc 818  
Qy 1131 tgaacctgtcgagggaagcaggagctgtgtggttcaacccctggattgtgttttcaat 1190  
Db 819 agccctggtcaaccagattggggagatcctggagctgaacctggatgtcatcatgtctct 878  
Qy 1191 tcacacggataaagaacaggggtgcacccacagggaagctcattaccacccctcttcccagg 1250  
Db 879 aaaca---atctcgatgaggagtcaacaag-----aagcatccgttcccctg 923  
Qy 1251 tccctgacattacgatctccctagcagcgtatgctgatcttttgaaatccctctagaaa' 1310  
Db 924 ccccaacctaccgcacggccctcaactactacgtgacatcactaaccccgccacgcac 983  
Qy 1311 ggcctctctgattgctctgcctcatgcatctgtacccagtgaaacagagagatgcg 1370  
Db 984 caatgtctctacgaactggcaagtagcctcagagccctcgaggcaggagcaactgca 1043  
Qy 1371 ctttttg-----tcatcacctctgggaagaatgagtattcaaaatgggtagttggaag 1424  
Db 1044 caagatggcgctcatctcagcggcagggcaaggagctgtacctgagctgggtggtgaagc 1103  
Qy 1425 tcagaggagctctttggagatcatggccgagtttccatcagcaaaaacccctcttgggt 1484  
Db 1104 ccggaggacacatccctagccatctccaagactaccatccactgctggcgccacct---cga 1160  
Qy 1485 gtctttgctgagtagccctcgtctaccgctcgatactattctatctcatctctcc 1544  
Db 1161 ccactgtgtgagctgtgcacgcctcagggcccgatactactccatgtgctcatctctc 1220  
Qy 1545 taagttgtctccctcaagaattcatgtgacgtgtgctttagtatatggttcaaaagccctac 1604  
Db 1221 caaggtccaccccaactcctgtcacatctgtgcctgcccgtggagtagcaagcgaagtc 1280  
Qy 1605 cggaaaggttcaaccgagagtggttgcacatggat-----gaagcatgcagttccctca 1658  
Db 1281 tggccgagtgaacaagggggtggccactagctggtgcttcgggccaaggaaccagcaggcga 1340  
Qy 1659 ggatagctg-----ggctcctattttgttcgaacgtcaaaacttcaagtaccagc 1709  
Db 1341 gaattggcgccgccccttgggtaccatgttgcgtgcgaaatctcagttccgcttgccttt 1400  
Qy 1710 tgacctccactcaactcaattatcatggtggacctggttacagggttagctctcttcagagg 1769  
Db 1401 caagtcaccacacacctgcatactatggtggcccgccactggattgcccctttcatggg 1460  
Qy 1770 atttctcaggaagaatagggccctcaagaaatggtgtctcaacttggcccgagctgct 1829  
Db 1461 cttcatccaggaaacagcttggcttcgagagcaaggcaggaggtgggagagagctgct 1520  
Qy 1830 ctttttccgattaggaatcgtataataggaacttattatgaagacgaactaaacaaactt 1889  
Db 1521 atactatggctgcgcgcctcggatgagagactatctgtaccgtgaagagctagccgctt 1580  
Qy 1890 cgtggaacgagaggtcatttctcgagctagttattgctcttttccagtgaaagggaagaa 1949  
Db 1581 ccacaaggacggtgcccctcaacgcgacttaattgtgccccttttcccggggagcaggccca 1640  
Qy 1950 ggaatatgtcaacataaagatgaggaagaagcaacgagatgtatgggaatgtgatcagg 2009  
Db 1641 ggtctatgtccagcaccttctgaagagagacagagggaacacactgtggaaagctgataccag 1700

Qy 2010 ggaecgt---tatctctatgtgtgtggtgaccccaagggaatggccagagatgtccatcg 2066  
Db 1701 gggcggtgccacatctatgtgtgcgggagatgctcgaataatggccaaagatgtgcaaaa 1760  
Qy 2067 cagcttgcataccattgcccaagaacaggagcccatggaatcatctgtgcgaagctgc 2126  
Db 1761 cacattctatgacattgtgctgagttcgggcccattggagcacaccaggtctggacta 1820  
Qy 2127 agtaaaagaactccaagtgtgaagaacgatatacttaagagatgtctgtgctgcg 2178  
Db 1821 tgttaagaagctgtagcacaaggccgcgtactactagatgtgtgagctag 1872

RESULT 9  
ID AAN81743 standard; DNA; 3435 BP.  
XX  
AC AAN81743;  
XX  
DT 19-OCT-1990 (first entry)  
XX  
DE Plasmid pAMP19.  
XX  
KW Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;  
KW industrial waste; ss.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3435  
FT /\*tag= a  
XX  
PN JP63044888-A.  
XX  
PD 25-FEB-1988.  
XX  
PF 12-AUG-1986; 86JP-0187713.  
XX  
PR 12-AUG-1986; 86JP-0187713.  
XX  
PA (AGEN ) AGENCY OF IND SCI TECH.  
XX  
DR WPI; 1988-094816/14.  
DR P-PSDB; AAP81334.  
XX  
PT Chimera fusion enzyme' gene - coding oxidation enzyme of cytochrome p-450  
PT and NADPH-cytochrome p-450 reduction enzyme  
XX  
PS Disclosure: ; p; Japanese.  
XX  
CC This plasmid is used in the prodn. of a chimeric fusion enzyme  
CC comprising the genes for the oxidation enzyme of cytochm. p-450 and the  
CC nicotinamide adenine dinucleotide phosphate (NADPH)-cytochm. p-450  
CC reduction enzyme. See also AAN81744-48.  
XX  
SQ Sequence 3435 BP; 816 A; 945 C; 940 G; 734 T; 0 other;

Query Match 7.3%; Score 192.8; DB 9; Length 3435;  
Best Local Similarity 49.0%; Pred. No. 1.6e-41;  
Matches 908; Conservative 0; Mismatches 872; Indels 72; Gaps 12;

Qy 354 aattaagctcactatatttttgggtactcagactggtgactgctgaaggattgttaagc 413  
Db 1629 aagaaacattatcgtattctatggtccacagcgggaacccgtgaggagtttgcacacg 1688  
Qy 414 attggcagaagaatttaaggcaaatgacaaagcaagcagttgttaaaagttagttgacctgga 473  
Db 1689 gcttccaagatccccaccctcagcggatgcgggcatgtcccgcacacccctgaagagta 1748  
Qy 474 tgactatgcacccgaggatgatcatcaataaagagaaataaagaaagagcttttgggtgtt 533  
Db 1749 tgacttggccgacctgacgacccctgcctga-----gatcgacaagtcctcgtgtagt 1799



PS Disclosure: ; p; Japanese.

XX This plasmid is used in the prodn. of a chimeric fusion enzyme  
 CC comprising genes for the oxidation enzyme of cytochrome p-450 and the  
 CC nicotinamide adenine dinucleotide phosphate (NADPH)-cytochrome p-450  
 CC reduction enzyme. See also AAN81743-85 and AAN81747-48.

XX Sequence 3453 BP; 821 A; 950 C; 947 G; 735 T; 0 other;

Query Match		7.3k;	Score 192.8;	DB 9;	Length 3453;
Best Local Similarity		49.08;	Pred. No. 1.6e-41;		
Matches 908;		Conservative 0;	Mismatches 872;	Indels 72;	Gaps 12;
Qy	354	aattaagctactatatttttggtagctacacagctggtactctgaagatttgcataaggc	413		
Db	1647	aaggaaacattatctattctatgctctccagacgggaaccgctgagagatttgcacacg	1706		
Qy	414	attggcagaagaatttaaggcaagttacaagaagcagttgtttaaagttagtgcacctgga	473		
Db	1707	gctgtccaagatgccaccgctacggatcggggcatgtccgcagacctgaagagta	1766		
Qy	474	tgactatcacgcagagatgatcaataatgaagagaataaagaagagctcttgggttt	533		
Db	1767	tgacttggccagctgagcagcctgctcga-----gatcgacaagtccctggtagt	1817		
Qy	534	tttcatggtagccacttatgtgtgtaggcacactgacaaatgctgcgagattttcaaa	593		
Db	1818	cttctgcatgccacatagcagagggcgacccacgagacaaatgcgagacttctatga	1877		
Qy	594	atggttcaactcagaacatgaaggggagtggtggttcagcaacttaacttatggttttt	653		
Db	1878	ctggctg-----caggagactgacgtggacctcaactcctgggtcgaatttgcgtatt	1928		
Qy	654	tggtttggtaaccgtcaatcacgagcatttcaacaagatcgcgtagatgtggatgaaca	713		
Db	1929	tggcttgggaacaagacctatgacatttcaatgccaatggcggaagtgtggaccagcg	1988		
Qy	714	actcggtaaacaggtgcaagcgcattgttcaagtgggctcggtgacgatgacaaatg	773		
Db	1989	gctggagcagcttggcgccacgcacattttagttgggcttggtagtgatgacgggaa	2048		
Qy	774	cattgaagatgattttactgcttggcgagaattgttggactgaattggatcagttgct	833		
Db	2049	cttggaaagattttcatcagtgtagggagcagttcttgcgcagctgtgtgcagattctt	2108		
Qy	834	caagatgagatgctgctcttcaagtgcgttacacgcgtatattgctactgttcttgaata	893		
Db	2109	-----tgggtatgaagccactgggagaggtcagacattcgcagtatgagctcgtgt	2162		
Qy	894	caggtagtgattcacgaaactacggt---cgcgctcttgatgataaacacataataac	950		
Db	2163	ccagaaacatggacgttagcgaaggtgtacacgggtgagatgggctctggaagagcta	2222		
Qy	951	tgttaacggcgtgttgcatttgatattcttcattcctcttgcagaaaccatttgttgcaca	1010		
Db	2223	cgagaaccagaaccccccttcgatcgaagaatccattccttgcgtgtgcacccgcaa	2282		
Qy	1011	aagagagctccacaacccccagctgtagatctctgtatatacatctggagttcgacatac	1070		
Db	2283	ccgaaagctgaaccaagca---ctgagcggcatctaaatgacactggagttggacatc	2339		
Qy	1071	aggtcttcccttcatatgagactggagatcatgttgggttttatgtctgagaactgcga	1130		
Db	2340	agactccaagatcaggtagaatctctggaga tcaagtggtgtgtaccacagccaatgactc	2399		
Qy	1131	tgaactgtcagagaagcaggaagctgttgggtcaacccccctgagttgtctgttttcaat	1190		
Db	2400	agcctgttcaaccagattggggagatcctctggagctgacctggagtgatcatcatgtctc	2459		
Qy	1191	tcacacgataaagaagcgggttcacccccaggggaagctcatataccacctctttccacgg	1250		
Db	2460	aaaca---atctcgtatgaggagttcaacaag-----aagcatcgttccccctg	2504		

Qy	1251	tccttgacaccttaagatctgcctcagcacgctatgctgatatcttttgaatcctctagaaa	1310		
Db	2505	cccaccacctaccgacgagccctcacctactactgacatcactaaccgcccagcac	2564		
Qy	1311	ggcttctctgattgctctgtccgtctcatgcatctgtaccacgtgaagcagagagattgcg	1370		
Db	2565	caatgtgcttacgaactggcacagtacgctcagagagccctcggagcaggaggacctgca	2624		
Qy	1371	ctttttg-----tcatacctctcgggaagaagaatgagtatccaatgggtagttggag	1424		
Db	2625	caagatggcgtcatcctcagcgggccaagagagctgtacctgagctgggtggggaagc	2684		
Qy	1425	tcagaggagtttttggagatcggcgagtttcttcacagcaaaacccccctcttgggtgt	1484		
Db	2685	cggaggcacatctcctagccatcctcccaagactaccatcactcggccaccat---cga	2741		
Qy	1485	gtctttgtcgtcagtagccctcgtctaccgacctgatactattctatctatctctctcc	1544		
Db	2742	ccactgtgtgagctgtgccacgctgagcccgatactactccattgacctctctc	2801		
Qy	1545	taagtttgcctcccaagaattcatgtgacgtgtgtcttagtatatggtcacaagccctac	1604		
Db	2802	caaggccacccccactcctgcacatctgtgcgtggccgtggagtagcgaagcgaagtc	2861		
Qy	1605	cggaaagggttcaccgagaggtgtgttcgacatggat-----gaagcatgcagttctcca	1658		
Db	2862	tggcagtagtaacaagggtgtggccactagctggtctcggccaaggaaccagcagcgca	2921		
Qy	1659	ggatagctg-----ggctcctatttttgttcgaacgtcaaaacttcagattaccgac	1709		
Db	2922	gaatggcgccgcgctgttaccatgttcgtgcgcaaatctcagttccgttcccttt	2981		
Qy	1710	tgacctcactcaactcaattatcatggtggacgtgtgacaggttagctctcttcagagg	1769		
Db	2982	caagtcacccacacactgtcatctggtggcccgccactggatctgcccccttcatggtg	3041		
Qy	1770	attcttcgcaaaaagaattggccctcaaggaataatggtctcaacttggcccagcagtgct	1829		
Db	3042	cttcatccagaaagagcttggcttcgagagcaaggaaggtgggagagacgtgct	3101		
Qy	1830	cttttctcggatgtgaggaatcgttaatatggaacttattatgaagcgaactaaacactt	1889		
Db	3102	atactatggtcggcgctcggatgaggaactatctgtaccgtgaagagctagcccgctt	3161		
Qy	1890	cgtggaaagagaggtcatttcggagctagttattgctctttcacgtgaaggggaaaaaa	1949		
Db	3162	ccaaagagcgggtgcccctcagcagcttaattgtggccttttcccggggagggcccaaa	3221		
Qy	1950	ggaatatgttcaacataaagatgaggaagaagcaacgagatgtatggaatgtgatatcagg	2009		
Db	3222	ggtctatgtccagcaccttctgaagagagacagaggaacacctgtggaagctgacccga	3281		
Qy	2010	ggacgggt---tatctctatgt	2066		
Db	3282	gggcggtgtccacacatctatgtgtcggggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	3341		
Qy	2067	cagttgtcatcaccattgcccagaacagagggacctgaatcatctgtctgcgaagctgc	2126		
Db	3342	cacattctatgacattgt	3401		
Qy	2127	agtaaaagaaactccaagtgtgaagacgatatctaagagatgtctgtgtgtgtgtgtgtgt	2178		
Db	3402	tgtaagaagctgatgacaaaggccgctactcactcatgattgtgtgtgtgtgtgtgtgtgt	3453		

RESULT 11  
 AAN81747  
 ID AAN81747 standard; DNA; 3399 BP.  
 XX  
 AC AAN81747;  
 XX  
 DT 19-OCT-1990 (first entry)



Dbb 3275 aagatgtgtcaaaacacattctatgatgacattgtgtggtgagttccggggcccatgagacacccc 3334  
Qy 2114 ctgccgaagctgcagtaagaagaccctccaagttgaaagacgatatcaatgaagatgtctgtgt 2173  
Db 3335 aggcgtgtgactatgttaagaagctgatgaccaagggccgctactactactagatgtgtgga 3394  
Qy 2174 gatcg 2178  
Db 3395 gctag 3399  
RESULT 12  
AAN70925  
ID AAN70925 standard; DNA; 2037 BP.  
XX  
AC AAN70925;  
XX  
DT 07-MAY-1991 (first entry)  
XX  
DE Sequence encoding NADPH cytochrome P-450 reductase.  
XX  
KW Yeast; Fpt; analgesic; antipyretic; ds.  
XX  
XX JP62104582-A.  
PN  
PD 15-MAY-1987.  
XX  
XX 31-OCT-1985; 85JP-0242772.  
XX  
PR 31-OCT-1985; 85JP-0242772.  
XX  
XX (AGEN ) AGENCY OF IND SCI TECH.  
XX  
XX WPI: 1987-173699/25.  
DR P-FSDB: AAP70578.  
XX  
XX Plasmid p-ARM1 simultaneously expressing rat hepato-cytochrome  
PT P-450MC - and NADPH-cytochrome P-450 reductase in yeast and yeast  
PT contg. p-RAM 1  
XX  
XX Disclosure; Fig 4; 9pp; Japanese.  
XX  
CC The sequence may be used to construct a plasmid which may  
CC transform a yeast expression system to produce both rat hepato-  
CC cytochrome P-450MC and NADPH cytochrome P-450 reductase (Fpt). This  
CC is useful in removal of organic compounds from toxic waste water.  
CC The yeast is capable of hydroxidising the p-position of  
CC acetanilide useful in the production of acetaminophenes which are  
CC antipyretics and analgesics.  
XX  
SQ Sequence 2037 BP; 481 A; 568 C; 588 G; 400 T; 0 other;

Query Match 7.2%; Score 191.2; DB 8; Length 2037;  
Best Local Similarity 49.0%; Pred. No. 3.3e-41;  
Matches 907; Conservative 0; Mismatches 873; Indels 72; Gaps 12;

Qy 354 aattaagctactatatttttggtaactcagactgtgactgaagatttgcataagc 413  
Db 231 aaggacattatcgatatctatgtgctccacgacgggaaccgctgaggatttgccaaacg 290  
Qy 414 attggcagaagaataaggcaagatacaagaagacagttgttaagtagttgacctgga 473  
Db 291 gctgtccaaagatgccaccgctacggatgctgaggatgtccgcagacctgaagagta 350  
Qy 474 tgactatgcagccgaggatgatcaataatgaagagaaataaagaagagtttgggtgtt 533  
Db 351 tgacttgccgacctgagcagctgctga -----gacgcagaagtccctggtagt 401  
Qy 534 tttaactgtagccacttatgtgtagtggtgagccaactgacaaatgctgcgagattttacaa 593  
Db 402 ctcttgatggccacatacgagagggcgacccacgacaaatgcgaggacttctatga 461

Qy 594 atggttactcagggaacatgaaggggagtggtgttcagcaactaaacttatgtgtttt 653  
Db 462 ctggctg-----caggagactgacgtggacactcactgggtcaagtttgcgtattt 512  
Qy 654 tgggttgggtaaccgtcaatacagacgacatttcaacaagatcgcggtagatgttgagagca 713  
Db 513 tgggtctgggaacaagacctatgacacttcaatgccatgggcaagtatgtggaaccagcg 572  
Qy 714 actcggtaacaaggtgcaaaagcgcattgttcaagtggggctcgcgtgacgagtgatcaatg 773  
Db 573 gctggagcagcttggcggccagcgcattcttgagttggcccttggtgagtagagcgga 632  
Qy 774 cattgaagatgattttactgcttggcggaattgttggactgaattggatcgaattgct 833  
Db 633 ctgggaagaggtttcatcaogtggaggagcagttctggccagctgtgtgcgagttctt 692  
Qy 834 caaagatgagagatgctgctccttcagtggtctacacggtatattgctactgttctcgaata 893  
Db 693 -----tggggtagaagccactggggaggtcgagcattcccgagtagtgagctggt 746  
Qy 894 caggtagtgattcacgaaactacggt---cgcgctctgtggtatataacacataaatac 950  
Db 747 caagaagacatggagctagccaaggtgtacacgggtgagatgggcccgtctgaagagcta 806  
Qy 951 tgcataacggcgatgttgcatttgatattctccatcctctgcagaaccattgttgcataca 1010  
Db 807 cgagaaccagaaaccccttcgatgtaagaatccattcctcgtcgtgcacgcgcaa 866  
Qy 1011 aagagagctccacaaacccagctgtgtagatcctgtatatacatctggaggtcgaatatc 1070  
Db 867 ccggaagctgaaccaggca---ctgagcggcatataatgcacctggagttggacatctc 923  
Qy 1071 aggcctctcccttatcatatgagactggagatcatgttggttttatgctgcgaaactgg 1130  
Db 924 agactccaagatcaggtagaatctggagatcacctggcgtgtgacccagccaatgactc 983  
Qy 1131 tgaactctcagggaagcagggaagcgtgtgggtcaacccctggattgtgttttcaat 1190  
Db 984 agccctggtcaaccagattggggagatcctggagctgacctgagctggtatcatctctct 1043  
Qy 1191 tcacacgataaagaagacgggttcacccacgggaagctcattaccacctctcttcccagg 1250  
Db 1044 aaaca---atctcgatgaggagtcaacaag-----aagcatctcgtttccctcg 1088  
Qy 1251 tcttgaccttaagatctgcccctagcagctatgctgattcttggaaacctcctcagaaa 1310  
Db 1089 cccacacctaccgcacggccctcactactactacctgacatcactaacccgccagcagc 1148  
Qy 1311 ggcctctctgattgctgtcgcgtcctatgcatctgtaccagtgaaagcagagagattgag 1370  
Db 1149 caatgtgcttacgaactggcacagtagcctcagagcctcgagcagcagagcactgca 1208  
Qy 1371 ctttttg-----tcatacactctgggaagaatgagtagttcaaaaatgggtagtggaag 1424  
Db 1209 caagatgctcatcctcctcagcgagggaagagagctgtacctgagctgggtggtggaagc 1268  
Qy 1425 tcagagagagcttttggagatcatggtccgagtttccatcagcaaaacccctcttgggt 1484  
Db 1259 ccggaggacatctctagcatctcccaagactaccatcactgctgagcagcagcagc 1325  
Qy 1485 gtctttgtcgtcagtagccctcgtctaccgctcgtactattctatctatctctctcc 1544  
Db 1326 ccacctgtgtgagctgtgcacgctcagggcccgataactactcctatgctcctctcc 1385  
Qy 1545 taagtgttctcctcaagaattcatgtgacgtgtgcttttagtatatggttcaaaagccctac 1604  
Db 1386 caaggtccaccaccaactcctgtcacatctgtgccgtggcgtggagtagcgaagcgaagtc 1445  
Qy 1605 cggaaaggttccaccgagaggtgtgttcacatggat-----gaagcatgcagttccctca 1658  
Db 1446 tggccgagtgaaacagggggtggccactagctggtctgggcccaggaaccagcaggcgga 1505  
Qy 1659 ggatagctg-----ggctcctattttgttcgaaacgtcaaaacttccaaagtaccagc 1709

Db 1506 gaatggcgccgcccgtgtaccatgttcctgcgcgaataatcagttccgcttccttt 1565  
QY 1710 tgaccctcaactcaattatcatgttggaacctggtacagaggttagctcctttcagagg 1769  
Db 1566 caagtccaccacacctcatcatgtgtggcccgccagctggattgccctttcatggg 1625  
QY 1770 atttctcaggaagaaatggccctcaaggaaatggtgtcctaacttggcccaagcagtgc 1829  
Db 1626 ctctatcaggaaacagagcttggtctcgagagcaaggcgaagggtggagagacgtctct 1685  
QY 1830 ctttttcggatagtagaactcgtaatatggaacttcattatgaagacgaactaaacaactt 1889  
Db 1686 atactatgctcgccgctcggtatgaggactatctgtaccctgaagagctagccgcttt 1745  
QY 1890 cgtgaaacagagagcatttcggagactagttattcccttttcacgtgaaggggaaaaagaa 1949  
Db 1746 ccacaagacggtgcctcaecagcagcttaattgccccttttcccgggagcagggcccaaa 1805  
QY 1950 ggaatatgtcaacataaagatgatggagaaacgaacgagatgtatggaatgtgatatacagg 2009  
Db 1806 ggtctatgtccagacccttctgaagagagacagggaacacacctgtggaagctgatccaga 1865  
QY 2010 ggacggt---tatctctatgtgtgtgtgtagtcccaaggaaatggccagagatgtccatcg 2066  
Db 1866 gggcgggtgccacatctatgtgtcggggatgctcgaatatggccaaagatgtgcaaaa 1925  
QY 2067 cacgttgataccattgcccaagaacagaggaccctgaatcatctgtcgcgaagctgc 2126  
Db 1926 cacattctatgacattgtgtgtgagttcgggcccatggagcacacccagctgtggaacta 1985  
QY 2127 agtaagaacatcccaagttgaagaaacgatatctaagagatgtctgtgtgacgt 2178  
Db 1986 tgttaagaagctgatgaccaaggccgcgtactcactactagatgtgtggagctag 2037

RESULT 13

AA8N1744  
ID AA8N1744 standard; DNA; 3453 BP.  
XX  
AC AA8N1744;  
XX  
DT 19-OCT-1990 (first entry)  
XX  
DE Plasmid pALP1.  
XX  
KW Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;  
KW industrial waste; ss.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3453  
FT /\*tag= a  
XX  
PN JP63044888-A.  
XX  
PD 25-FEB-1988.  
XX  
PF 12-AUG-1986; 86JP-0187713.  
XX  
PR 12-AUG-1986; 86JP-0187713.  
XX  
PA (AGEN ) AGENCY OF IND SCI TECH.  
XX  
XX WPI; 1988-094816/14.  
DR P-PSDB; AAP81335.  
XX  
PT Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450  
PT and NADPH-cytochrome p-450 reduction enzyme  
XX  
PS Disclosure; ; P; Japanese.  
XX  
XX This plasmid is used in the prodn. of a chimeric fusion enzyme  
CC comprising the genes for the oxidation enzyme of cytochm. p-450 and the

CC nicotinamide adenine dinucleotide phosphate (NADPH)-cytochm. p-450  
CC reduction enzyme. See also AA8N1743 and AA8N1745-48.  
XX  
SQ Sequence 3453 BP; 817 A; 950 C; 946 G; 740 T; 0 other;  
  
Query Match 7.2%; Score 191.2; DB 9; Length 3453;  
Best Local Similarity 49.0%; Pred. No. 4.3e-41;  
Matches 907; Conservative 0; Mismatches 873; Indels 72; Gaps 12;  
  
QY 354 aattaagctcaactatatttttggctactcagactggtactgctgaaggatttggctaaagc 413  
Db 1647 aaggaaactattatctattctatgctcccgagcggaacccgctgaggaattggccaacgc 1706  
QY 414 attgcagagaagaaattaaggcaaaagtacaagaaacagctgtgttaaagttagtgaacctgga 473  
Db 1707 gctgtcccaaggatgccaccgctacgggtatcggggcatgtccgcagacccctgaagagta 1766  
QY 474 tgactatgcagccgaggtatgataatataagagaaaaattaaagaaagagctctttggtgtt 533  
Db 1767 tgactggccgacctgagcagcctgcctga-----gatcgacaatgccctggtagt 1817  
QY 534 ttctatgtagccacttatgtgtgtagcgaactgacaaatgctgcgagattttacaa 593  
Db 1818 cttctgcatggccacatacggagaggcggaaccccgacaatgcgcaggacttctatga 1877  
QY 594 atggttcaactcaggaaacatgaaggaggagagtggttcgaacaactaatattggtgtttt 653  
Db 1878 ctggctg-----caggagactgaactggacactcactcctcctcctcctcctcctt 1928  
QY 654 tggttgggttaaccgtcaatcagcagcatttcaacaaagatcgcggtagatgtggtagagca 713  
Db 1929 tggctctgggaacaagacctatgacacttcaatgccatgggcaagtatgtgagaccagcg 1988  
QY 714 actcgttaacaaggtgcaaaagcagcttgttcaagtgggctcgtgacgatgatcaatg 773  
Db 1989 gctggagcagcttggcccgacgcatctttagttggccttggtagatgacgagcgaa 2048  
QY 774 cattgaagatgattttactgcttggcgagaattgttggactgaattggatcagttgct 833  
Db 2049 ctgggaagaggatttcaatcaactggaggagcagttctcctggcagctgtgtgcgagtctt 2108  
QY 834 caaagatgaggatgctgctcctcagtggtcacccgtatatattgctactgtcctgaata 893  
Db 2109 -----tggggtagaagccactgggagggagtcgagcattcccgatgagctggtgt 2162  
QY 894 cagggtagttacacgaaactacggt---cgcggtcgtggtatgataaacaacataaatac 950  
Db 2163 ccacgaagacatggagctagccaaggtgtacacgggtgagatggcgctcgaagagcta 2222  
QY 951 tgctaacggcgatgttgcatttgatattctccactcttcgagaacacattgttgcctcaaca 1010  
Db 2223 cgagaaccagaaacccctctcgatgctaagaatccattcctcctggctgtgtccacgcca 2282  
QY 1011 aagagactccacaaccccaagctctgatagatccctgtatacatctggagctcgacatctc 1070  
Db 2283 ccggaagctgaaccaaggca---ctgagcggcatctaatacgacctggaggttggaatctc 2339  
QY 1071 aggtctctcccttacatatgagactggagatcatgttgggttttatgtctgagaactcgga 1130  
Db 2340 agactccaagatcaggtagaattcggagatcacgtggctgtgtaccacgccaatgactc 2399  
QY 1131 tgaactctcgagggaagcagggaagcgttgggtcaacccctggagtttgcgttttcaat 1190  
Db 2400 agcctgttcaaccagattggggagatcctggagctgacctggatgcatcatgtctct 2459  
QY 1191 tcacacgataaagaagcgggtcccccagggagagctcattaccacctcttctccagg 1250  
Db 2460 aaaca---atctcgatgaggagtcacaag-----aagcatccggttccctcg 2504  
QY 1251 tcttgcaccttaacgatctgccttagcagcagctatgctgatcttttgaatcctctagaaa 1310  
Db 2505 ccccaaccctacgcacggccctcacctactactgacatcactggaacataaccgcccagcac 2564



Qy 1311 ggcttctctgattgctctgctcgtcattctgtaccagtgaaagcagagagattgctg 1370  
 Db 2565 caatgtctctacgaactggaacagtacgtcctcagagccctcgagcaggaacctgca 2624  
 Qy 1371 ctttttg-----tcacacctctgggaaagaatgagttatccaatgggtagttggaag 1424  
 Db 2625 caagatggcgtcattctcctcagcgagggcgaagagctgacactgagctgggtggtggaagc 2684  
 Qy 1425 tcagagagagctcttttggagatcagcgagcttccatcagcaaaacccctcttgggtg 1484  
 Db 2685 ccggaggccacatctcagccatcctcgaagactacccaactcgtcgccaccocat---cga 2741  
 Qy 1485 gttctttgctcagtagccctcgttaccgctcgtacactattctctcctctccc 1544  
 Db 2742 ccactgtgtgagctgtgcacgctcagcgccgatactactcattgctcctcctc 2801  
 Qy 1545 taagtgttctcctcaagaattcatgtgacgtgtgctttagtatatgtgtcaaacccctac 1604  
 Db 2802 caaggtccaccccaactcctgtcacatctgtgccgtggcgtgagtagcgaagcgaagtc 2861  
 Qy 1605 cggaaggttaccgagagagtggttcacatgagat-----gaagcatgagttcctca 1658  
 Db 2862 tggccagtgaaacaaaggggtggccactagctggcttcggccaaaggaaacagcaggcga 2921  
 Qy 1659 ggatagctg-----ggctcctattttgttcgaagctcaaaacttcaagtaccagc 1709  
 Db 2922 gaatggcgccgcccctgtgtaacctgttgcgtgcgaatactcagttccgttgcctt 2981  
 Qy 1710 tgacctccaactccaattatcatggtggacctggtacaggggttagctctcttcagagg 1769  
 Db 2982 caagtcacacacactctcatctggtggcccgccgactgggtgggagagacgtctgt 3041  
 Qy 1770 atttctcaggaagaatggccctcaagaaatggtcctcaacttggcccgagcagtgct 1829  
 Db 3042 ctctatccaggaacagagcttggtctcgagagcaaggcaggggtgggagacgtctgt 3101  
 Qy 1830 ctttttcgagtaggaatcgtaattgacttctttagagacgaactcaaaactt 1889  
 Db 3102 atactatggtcgccgctcggtgagactatctgacgtgaagagtagcgcgtt 3161  
 Qy 1890 cgtggaacagagagctatttcgagctagttattgccttttcacgtgaaggggaaagaa 1949  
 Db 3162 ccacaagagcgtgcccctcagcagcttaattgtgcttttccgggagcagcccaaa 3221  
 Qy 1950 ggaatatgtcaacataagatgatggagaacacgagatgtatggaatgtgatcagg 2009  
 Db 3222 ggtctatgtccagacacctctgaaagagacagggaaacacctgtggaagctgatccaga 3281  
 Qy 2010 ggaaggt---tatctctatgtgtgtggtgatgccaaagggaatggccagagatgtccatcg 2066  
 Db 3282 gggcggtgccacatctatgtgtcggggagctgcgaataatggccaaagatgtgcaaaa 3341  
 Qy 2067 cagctgtgataccattgccaaagacagggaccctatgaatcatctgtcgcgaagctgc 2126  
 Db 3342 cacattctatgacattgtggtgagttcgggccccttgagacacccagctgtggaacta 3401  
 Qy 2127 agtaagaacacccaaagttgaagaacgatatacgaagatgtctggtgatcg 2178  
 Db 3402 tgttaagaagctgatgaccaagggccgtactcactagatgtgtggaagctag 3453

RESULT 14

AA70605  
 ID AA70605 standard; cDNA; 2450 BP.

XX  
 AC  
 AA70605;

XX  
 DT 26-APR-1991 (first entry)

XX  
 DE Plasmid pRF1 encoding rat liver NADPH cytochrome P450 reductase.

XX  
 KW P-450MC; Fpt; Saccharomyces cerevisiae AH22; ds.

XX Rattus sp.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 41..2077  
 FT /\*tag= a  
 PN JP62019085-A.  
 XX  
 PD 27-JAN-1987.  
 XX  
 PF 05-JUL-1985; 85JP-0146653.  
 XX  
 PR 05-JUL-1985; 85JP-0146653.  
 XX  
 PA (AGEN ) AGENCY OF IND SCI TECH.  
 XX  
 DR WPI; 1987-062501/09.  
 DR P-PSDB; AAP70380.  
 XX  
 PT New plasmid typically pRF1 - has total coding region of rat liver  
 PT NADPH cytochrome p-450 reductase gene  
 XX  
 PS Disclosure; Fig 4; 14pp; Japanese.  
 XX  
 CC The rat liver NADPH-cytochrome P-450 reductase gene may be used to  
 CC transform a yeast expression system (S.cerevisiae AH22) for the  
 CC production of rat liver Fpt and P-450MC of high oxidation activity.  
 XX  
 SQ Sequence 2450 BP; 572 A; 689 C; 493 T; 0 other;

Query Match 7.1%; Score 187.6; DB 8; Length 2450;  
 Best Local Similarity 48.7%; Pred. No. 3.4e-40;  
 Matches 913; Conservative 0; Mismatches 889; Indels 72; Gaps 12;  
 Qy 354 aataagctcactatatttttggactcagactggtactgctgaaggatttggtaagc 413  
 Db 271 aaggaaactattcgtattcttgcctccagacgggaaacgctgagaggtttgccaacg 330  
 Qy 414 atggtcagaagaattaaaggcaagatacaagaacagctgtttaaagtagtgacctgga 473  
 Db 331 gctgtccaaaggatgccaccgctacggggtacggggtgctgcgcgacccctgaagacta 390  
 Qy 474 tgactatgcagccgaggtgatgataatgaagagaattaaagaagagctcttgggtgtt 533  
 Db 391 tgacttgcgaccgagcagcagcgcctgctga-----gacgcagaagctcctgtagt 441  
 Qy 534 ttctatggtagccacttatgtggtgagccaaactgacaatgctgcgagattttcaaa 593  
 Db 442 ctcttgcatggccacatacggagggcgacccacgggaaatgacgagactctatga 501  
 Qy 594 atggttactcaggaacatgaaggggagagtggttccagcaactaacatctggttttt 653  
 Db 502 ctggtgtg-----caggagactgacgtgacccactcactgggttcaagttgctgatt 552  
 Qy 654 tggtttggtaaacgctcaatcagcagcatcttcaacaagatcgcggtagatgtggatgagca 713  
 Db 553 tggcttgggaacaagacactatgacacttcaatgcatgaggaagtagtggaaccagag 612  
 Qy 714 actcgttaacaaggttgcaagcgcatttccaagtggggctcgggtgacgatgatactgct 773  
 Db 613 gctggagcagctggcgccagccgatcttggagtggtggccttgggtgagacgggaa 672  
 Qy 774 cattgaagatgattttactgcttgcgagaattgttggactgaattggatcagctgct 833  
 Db 673 cttggaagaggatttcatcactggtggaggagcagttctggtgagagcttctt 732  
 Qy 834 caaagatgaggtgctcctcctcagtggtctacacgctatattgctactgcttctctgata 893  
 Db 733 -----tggggtagaagccactggggagagctcagcattcgcgaatgatgagctgtgt 786  
 Qy 894 cagggttagtgattcacgaaactacggt---cgcggtctctggtatgataaacacataaac 950

Db 787 ccacgaagacatggcgtagcagcaaggtgtacacgggtgagatgcgcgtctgaagacta 846  
Qy 951 tgcctaaccggcagtgtgtgaattgatatctcattctccactctgcagaaacattgtgtgctcaaca 1010  
Db 847 cgagaaacagaaacccccctctcgatgctaagaatccattccttggtgtgtgcaccgcca 906  
Qy 1011 aagagagctcccaaaccaacgaatcgatagatccctgtatcacatctcgaggtcgacatctc 1070  
Db 907 ccggaagctgaaccaagga---ctgagcggcatctaataatgcacctggaggtggacatctc 963  
Qy 1071 agcctctcccttaccatatgagactggagatcatgtgtggtgtttatgtctgagaactggga 1130  
Db 964 agactccaagatcacggtatgaatctggagatcaocgtgctgtgtacccagccaatgactc 1023  
Qy 1131 tgaactgtcggagggaagcaggaaagctgtgtgggttcaacccctggattgtgttccaat 1190  
Db 1024 agcctgtgtcaaccagattggggagatcctggagctggagctgaacctggatgtcatctctct 1083  
Qy 1191 tcacacgataaaagacgggtcaccacagggaagctcattaccacctcttcccagg 1250  
Db 1084 aaaca---atctcgatggggagtcacaag-----aagcatccogttcccctg 1128  
Qy 1251 tccctgcaccttaecgatctgccttagcagcgtatgctgatcttttgaatccctccctagaaa 1310  
Db 1129 cccaaccactaccgcagcgcctcacctactactactcagacatacctaaccgcagcagc 1188  
Qy 1311 ggcctctctgattgtctgtcgcgtcatgctatctgtatcttttgaatccctccctagaaa 1370  
Db 1189 caatgtctctacgaactggcagactagcctcagcagcctcgagcagcagcagcactgca 1248  
Qy 1371 ctttttgcatacctct-----gggaagaatgagtattcaaaatgggtagttgggaag 1424  
Db 1249 caagatggcgtcatcctcaggcggagcgaagagctgtacctgagctgggtggtggaagc 1308  
Qy 1425 tcagaggagctcttttggagatcagcgcaggtttccatcagcaaaacccctcttgggtg 1484  
Db 1309 cggaggagcaatctcagcactcctcagagactaccatacctcagtcggccaccat---cga 1365  
Qy 1485 gtcttctgtcgcgtagccccctcgcttaaccgctcgtactactatctatctcctctccc 1544  
Db 1366 ccacctgtgtgagctgtgtgccacgcctgcagcgcgcgatactactcctccttgcctatcctc 1425  
Qy 1545 taagtttgcctcccaagaattcatgtgacgtgtgcttttagtatatgttcaaaagccctac 1604  
Db 1426 caaggtccaccccaactccgtgcacatctgtgccgtgcccgtggagtacgaagcgaagtc 1485  
Qy 1605 cggaaaggttccaccgaggaggtgtgtcgacatggat-----gaagcatgcagttccctca 1658  
Db 1486 tggcccaatgaacaagggggtggccactagctggcttcgggccaaaggaaaccaagcaggcga 1545  
Qy 1659 ggaatagctg-----ggctcctattttgttcgaacgtcaaaacttcaagttaccagc 1709  
Db 1546 gaatggcggcgcgcctcgtgtaccatgttgctgcgaaaatctcagttccgcttgcttt 1605  
Qy 1710 tgacctccaactccaattatcatgtgtggacctggtacaggggttagctcctttcagagg 1769  
Db 1606 caagtccaccacacgtctcatatggtggcccgccgactggattgcccccttctatgg 1665  
Qy 1770 atttctcaggaaagaatggccctcaaggaataatggtgtctcaacttggccagcagctgct 1829  
Db 1666 ctctaccaggaaacagcttggcttcgagacgaagcaggaggtgggagagacgtcgt 1725  
Qy 1830 ctttttcggatgtagaatactgtaatatggaacttctatttatgaagcagcaactaaacaatt 1889  
Db 1726 atactatggtcgcgcgtcggatgagactatctgacogtgaagagctagcccgctt 1785  
Qy 1890 cgtgaaacaggagactattccgagctagttattgcctttttcacgtgaagggaagaaagaa 1949  
Db 1786 ccacaaggacggtgcccccaacgcagcttaatgtggcccttttcccggggagcaggcccccaa 1845  
Qy 1950 ggaatatgtcaacataagatgattgagaaagcaacgcgattgtatggaatgtgatccagg 2009

Db 1846 ggctctatgtccagcaccttctgaagagagacaggggaacacctgtggaagctgatccacga 1905  
Qy 2010 ggaacgt---tatctctatgtgtgtgtatgccaaaggaatggccagagatgtccatcg 2066  
Db 1906 gggcgggtgccacatctatgtgtcggggatgctcgaaaataggccaaagatgtgcaaaa 1965  
Qy 2067 cagctgtacataccattgcccagaacagcaggaccatggaatcatctgtgcggaagctgc 2126  
Db 1966 cacattctatgacattgtgctgagttcgggcccataggagcacacccagcgtgtggacta 2025  
Qy 2127 agtaagaacatcccaagtttgaagaacgatatctaaagatgtctgtgtcgaatgtagc 2186  
Db 2026 tgttaagaagctgtagaccaaggcgcgtactcactagatgtgtgagctagagctacc 2085  
Qy 2187 ttgccaagtccccct 2200  
Db 2086 agcctcccaacct 2099

RESULT 15  
AAN81745  
ID AAN81745 standard; DNA; 3489 BP.  
XX  
AC AAN81745;  
XX  
DT 19-OCT-1990 (first entry)  
XX  
DE Plasmid pALP17.  
XX  
KW Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;  
KW industrial waste; ss.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3490  
FT /\*tag= a  
XX  
PN JP63044888-A.  
XX  
PD 25-FEB-1988.  
XX  
PF 12-AUG-1986; 86JP-0187713.  
XX  
PR 12-AUG-1986; 86JP-0187713.  
XX  
PA (AGEN ) AGENCY OF IND SCI TECH.  
XX  
DR WPI; 1988-094816/14.  
XX  
DR P-PSDB; AAP81336.  
XX  
PT Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450  
PT and NADPH-cytochrome p-450 reduction enzyme  
XX  
PS Disclosure; ; p; Japanese.  
XX  
CC This plasmid is used in the prodn. of a chimeric fusion enzyme  
CC comprising genes for the oxidation enzyme of cytochrome p-450 and the  
CC nicotinamide adenine dinucleotide phosphate (NADPH)-cytochrome p-450  
CC reduction enzyme. See also AAN81743-84 and AAN81746-48.  
XX  
SQ Sequence 3489 BP; 813 A; 964 C; 955 G; 757 T; 0 other;

Query Match 6.4%; Score 170.4; DB 9; Length 3489;  
Best Local Similarity 48.3%; Pred. No. 1.7e-35;  
Matches 894; Conservative 0; Mismatches 886; Indels 72; Gaps 12;

Qy 354 aattaagctcactatatttttggctactcagactggtactgctgaaggatttctaagc 413  
Db 1683 aaggaaacattatcgtattctatgtctccacgacgggaacccgtgaggatttggcacaacg 1742  
Qy 414 attggcagaagaataaaggcgaagtacagaagaagcagttgttaagtagttgacctgga 473  
Db 1743 gctgtccaaggatgccaccgctacgggatcggggcatcggggcatgtccgcagaccctgaagagta 1802



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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 12:28:30 ; Search time 2203.48 Seconds  
(without alignments)  
12918.460 Million cell updates/sec

Title: US-09-486-757-10  
Perfect score: 2649  
Sequence: 1 cggcagcagctgttagtat.....ttttgagaaaaa 2649

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues  
Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estfun:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estom:\*  
5: em\_estpl:\*  
6: em\_estba:\*  
7: em\_estov:\*  
8: em\_estov:\*  
9: em\_hic:\*  
10: gb\_est1:\*  
11: gb\_est2:\*  
12: gb\_hic:\*  
13: gb\_gss:\*  
14: em\_gss\_fun:\*  
15: em\_gss\_hum:\*  
16: em\_gss\_inv:\*  
17: em\_gss\_pln:\*  
18: em\_gss\_pro:\*  
19: em\_gss\_rod:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	394.4	14.9	659	10	AT1730999
2	394	14.9	775	11	BF003997
3	378.2	14.3	659	10	AW695744
4	371.4	14.0	658	10	AW256561
5	366.6	13.8	683	10	AW398515
6	357.6	13.5	824	11	BC319913
7	350.6	13.2	559	11	BC362645
8	350.2	13.2	770	11	BF266609
9	346.2	13.1	681	11	BF266609
10	343.2	13.0	903	11	BF266609
11	338.8	12.8	680	11	BF266609
12	336	12.7	605	10	AW931765

13	333	12.6	626	11	BG645950
14	325.6	12.3	528	11	BI424233
15	325	12.3	590	10	BE461594
16	322.4	12.2	548	11	BE204346
17	317.8	12.0	546	11	BF637910
18	316.6	12.0	782	10	BE413142
19	316	11.9	745	11	BF598829
20	314.2	11.9	706	10	AW584757
21	310.4	11.7	699	10	AL504215
22	306.4	11.6	584	11	BI308367
23	306	11.6	610	10	BE443158
24	305.4	11.5	580	10	AW036681
25	304.8	11.5	764	11	BF256187
26	304.6	11.5	604	10	AW869841
27	303.8	11.5	758	11	BG647603
28	302.8	11.4	530	10	AW030326
29	302.2	11.4	547	10	AW979914
30	297.8	11.2	517	10	BE608297
31	296.4	11.2	668	10	AW685470
32	296	11.2	698	13	BH012931
33	294.2	11.1	667	11	BG045230
34	294	11.1	656	11	BG452152
35	292.8	11.1	449	11	BF005171
36	292.2	11.0	594	10	AW219488
37	290.4	11.0	584	10	AW441648
38	289.6	10.9	616	10	AW255332
39	289.2	10.9	606	10	BE364291
40	289	10.9	612	11	BF010242
41	286.4	10.8	696	10	AL503659
42	286.4	10.8	767	10	BE412849
43	286.2	10.8	500	11	BG726758
44	285.6	10.8	584	10	AW217142
45	282.4	10.7	670	11	BG451984

ALIGNMENTS

RESULT	1
AT1730999	AT1730999
LOCUS	BNLGH18371 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AL035356) NADPH-ferrihemoprotein reductase ATRI [Arabidopsis thaliana], mRNA sequence.
DEFINITION	thaliana], mRNA sequence.
ACCESSION	AT1730999.1 GI:5049851
VERSION	EST.
KEYWORDS	upland cotton.
SOURCE	Gossypium hirsutum
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE	1 (bases 1 to 659)
AUTHORS	Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.
TITLE	ESTs from developing cotton fiber
JOURNAL	Unpublished (1999)
COMMENT	Contact: Ben Burr Biology Department Brookhaven National Laboratory Upton, NY 11973, USA Tel: 516-344-3396 Fax: 516-344-3407 Email: burr@bnl.bnl.gov Seq primer: T3 Primer. Location/Qualifiers 1. .659 /organism="Gossypium hirsutum" /cultivar="Acala Maxxa" /db_xref="taxon:3635" /clone_lib="Six-day Cotton fiber" /tissue_type="Immature fiber" /dev_stage="Six days post anthesis" /lab_host="XL1-Blue"
FEATURES	source

with Sinorhizobium meliloti Unpublished (1999) Contact: VandenBosch K Department of Biology Texas A&M University College Station, TX 77843-3258, USA Tel: 409 845 7707 Fax: 409 845 2891 Email: kate@mail.bio.tamu.edu Texas A&M University name: T267798e TIGR sequence name: MTIAZ18TK More information is available at: http://chryslie.tamu.edu/medicago Seq primer: SKmod (CTA gAA CTA gtg gAT CC).		JOURNAL COMMENT	
FEATURES		source	
1. .775			
/organism="Medicago truncatula"			
/cultivar="genotype A17"			
/db_xref="taxon:3880"			
/clone_lib="KVI"			
/issue_type="Seedling roots"			
/dev_stage="24 hours post-inoculation with Sinorhizobium meliloti"			
/lab_host="E. coli strain XL0LR"			
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."			
BASE COUNT 198 a 163 c 181 g 233 t			
ORIGIN			
Query Match 14.9%; Score 394; DB 11; Length 775;			
Best Local Similarity 71.8%; Pred. No. 2e-86;			
Matches 536; Conservative 0; Mismatches 195; Indels 15; Gaps 1;			
Qy 1381	tcacctctgggaagaatgagattcacaatgggtagttgggaagtcagagagcttttg 1440		
Db 12	TCCTCTCAGGGTAAGAGTGAATACTCCAATGGTGTGTGGAGGCCATAGAACTCTTCTT 71		
Qy 1441	gagatcatgcccaggtttccatcagcaaaacccccctcttggtgtgtctttcttcagta 1500		
Db 72	GAGGTGATGCTGATTTTCCATCAGCAAAACACCCTTGGTGTGTGTGTGCTGCATA 131		
Qy 1501	gccccctgctaccgctcgatactattctatctcatctctctcaagtittgctccctca 1560		
Db 132	CCCCCTCGTTTAAACACTCGTTATTATTCTATTTATCTATCTCCCTAGGTTTGCCTCCACAA 191		
Qy 1561	agaattcatgtgcgtgtcttagtatatgttcctcaagccctaccggaagggttccacga 1620		
Db 192	AGGTCACACTAACTTGTGCCCTGGTAGAGGTCCCAACTCCCAACTGGCGAGAATTACAAA 251		
Qy 1621	ggagtgtgttcacatggatgaagcatgcagttccc-----tcaggatagtc 1665		
Db 252	GGAGTATGTTCAACCTGGATGAAGATGCTATTCCCTCAGAGGAAGCGTGACTGTAGC 311		
Qy 1666	tgggctctctatttttgcgaacgtcaaaactcaagtaccagctgacccctcaactcca 1725		
Db 312	TGGGCTCCCAATTTTATCAGGCCATCGAAATTTCAAGCTACCTGCTGATCTCTTCAATTGCT 371		
Qy 1726	attatcatggtggacctggtacaggttagctctcttcacagagattctcgcagaaaga 1785		
Db 372	ATTATTATGTTGGACTGCTGCTGTTTATGACACCTTTTAGGGGATTTTACAGGAGAGA 431		
Qy 1786	atggccctcaagaaatggtgctcaacttggccagcagtgctcttttccttgatgtagg 1845		
Db 432	TTTGCTCTCAAGAGGACGGTGTCAACTTGGTCTCGCATTTACTATTCTTCGGGTGCAGG 491		
Qy 1846	aatcgtaatatgacttcatattatgaagcgaactaaacaacttcgtggaacgaggtc 1905		
Db 492	AACCGTCAATGATTTTATATATGAGGAAGAGCTGAATAATTTGTGTGGAACAAGGTCT 551		

JOURNAL COMMENT	with Sinorhizobium meliloti Unpublished (1999) Contact: VandenBosch K Department of Biology Texas A&M University College Station, TX 77843-3258, USA Tel: 409 845 7707 Fax: 409 845 2891 Email: kate@mail.bio.tamu.edu Texas A&M University name: T267798e TIGR sequence name: MTIAZ18TK More information is available at: http://chrystie.tamu.edu/medicago Seq primer: SKnod (CTA gAA CTA gtg gat CC).	
FEATURES	Location/Qualifiers	
source	1. .775 /organism="Medicago truncatula" /cultivar="genotype A17" /db_xref="taxon:3880" /clone="pkV1-14C12" /clone_lib="KV1" /tissue_type="Seedling roots" /dev_stage="24 hours post-inoculation with Sinorhizobium meliloti" /lab_host="E. coli strain XL0LR" /note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."	
BASE COUNT	198 a 163 c 181 g 233 t	
ORIGIN		
Query Match	14.9%; Score 394; DB 11; Length 775;	
Best Local Similarity	71.8%; Pred. No. 2e-86;	
Matches 536; Conservative	0; Mismatches 195; Indels 15; Gaps 1;	
Qy	1381	tcacctctgggaaagaatgagattatccaaatgggtagttgggaagtcagagagatctttg 1440
Db	12	TCTCCTCAGGGTAAAGGATGATCTCCAAATGGGTGTTGGGAAGCCATAGAATCTCTCT 71
Qy	1441	gagatcatgcccaggtttccatcagcaaaacccctcttggtggtctcttttgcgtcagta 1500
Db	72	GAGGTGATGCTGATTTTCCATCAGCAAAACCCCTTGGTGTGTTTTTGTGTCCTA 131
Qy	1501	gccctcgtctaccgcctcgatactattctatctatctcctcctcctcctcctcctca 1560
Db	132	GCCCTCGTTCACACCTGCTGTTATTATTTTCATCATCTCTCTAGGTGTGCCCCACAA 191
Qy	1561	agaattcatgtcagctgtgcttttagtatatgttcaagccctaccggaaggttcaccga 1620
Db	192	AGGTACACGTAACTTGTGCCCTGGTAGAAGGTCCAACCTGCCAAGATTCACAAA 251
Qy	1621	ggagtgtgttcgacatggatgaagcatgcagttcc-----tcaggatagc 1665
Db	252	GGAGTATGTTCAACCTGGATGAGAAATGCTATTCCTCAGAGAAACCGTGACTGTAGC 311
Qy	1666	tgggtcctctattttgttcgaaacgtcaaaacttcaagttaccagctgacccctcaactcca 1725
Db	312	TGGGTCCCATTTTTATCAGGCCATCGAATTTCAAGCTACCTGCTGATCCTTCAATTCCT 371
Qy	1726	attatcatgttggacctggtacaggggttagctcctttcagaggattctcagaggaaga 1785
Db	372	ATTATTATGGTTGGACCTGGTACTGGTTTAGCACCTTTTAGGGGATTTTACAGGAGAGA 431
Qy	1786	atggccctcaagaaaaatggtgtcctaacttgcaccaagctgctcttttccgattag 1845
Db	432	TTTGTCTCAAGAGGACCGGTGTTCAACTTGGTCTGCAATTACTATCTTCGGGTGCAGG 491
Qy	1846	aatcgtaatatggacttcatttatgaagacgaactaaacaactctcggaacgagagtc 1905
Db	492	AACCGTCAATGGATTTTATATATGAGGAAGAGCTGAATAATTTTGTGGAACAAGTTCT 551



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/organism="Medicago truncatula"
/cultivar="genotype AL7"
/db_xref="taxon:3880"
/clone="KV2-5G11"
/clone_lib="KV2"
/tissue_type="Seedling roots"
/dev_stage="2 days post-inoculation with Sinorhizobium meliloti"
/lab_host="E. coli strain SOLR"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
cDNA was prepared from polyA+ enriched RNA. The
cDNA was directionally ligated into the Unizap XR vector
from Stratagene and packaged using Gigapack III Gold
packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-Zap phage using
Ex-assist helper phage and propagated in SOLR cells."

BASE COUNT      156 a   138 c   158 g   206 t
ORIGIN

Query Match      14.0%; Score 371.4; DB 10; Length 658;
Best Local Similarity 73.0%; Pred. No. 7.3e-81;
Matches 477; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 699 agatgtggatgagcaactcggttaaacagaagtgcaagcgcatgttcaagtggggctcgg 758
Db 6 AGTTGTTGACGATTATCTCAGTGTTCAAAGGGCAAGCGTCTGTTCACCTTGGAAATGGG 65

QY 759 tgacgatgatcaatgcattgaagatgattttactgcttggtggcgagaattgttggtgactga 818
Db 66 TGATGATGATCAATCCATTGACGATGATTTAATGCGTGAAGAAGATCTCTGTGGCCTGA 125

QY 819 attggaatcagttgcctcaagaatgaggatgctgctcctcagtggtgcacaccgtatatgc 878
Db 126 GTTGGATCAGTTGCTCCGAGTGGAGATGATGTAATACTGTGTCTACTCCCTATTACACG 185

QY 879 tactgttcctgaatacaggttagtgattcacgaacacagtcgcggtccttgatgataaa 938
Db 186 TGCTATTTCTGAATATCAGTAGTGTTCACGACCCCACTGTTCACGCCGCTCTACGAGAA 245

QY 939 acacataaatactgtaacggcgatgtgttcatttgatatctccatccttcgcagaacct 998
Db 246 TCACCTTTAACGGCGCAAAATGGGGTGTCTGATTGTATATTCATATCCCTGTAGGCGGAA 305

QY 999 tgttctcaacaaagagactccacaaacccaaagctcgtatagatcctgtatcacatctgga 1058
Db 306 TGTGCGCTGTCGAAGGAGCTTCATAAACTCAGTCTGACCGTCTGTGATACATTTGGA 365

QY 1059 gttcgacatatcaggtctctcccttcacatatgagactgagatcatgttggtgtttatgc 1118
Db 366 GTTTGATGATATCAGGACCGCGCTAACATACGAAACTGGAGACCATGTGGGTGTTTATGC 425

QY 1119 tgagaactcgtatgaactgtcgaagaagcagggagctgttggttcaaccctcgattt 1178
Db 426 TGATAACTGTGATGAACCTGTTTAAAGAGCTGGGAAGTTGTTGGGTTCAGGATTTAGATTT 485

QY 1179 gctgttttcaattcacaggaataaagaagacgggtccaccgccgaagcctcattaccacc 1238
Db 486 GCTGTTTTCTTTCACATGTAANTAGAGATGGCACTTCCCTAGGTGGTGTCTCTCTAC 545

QY 1239 tccittccaggtcccttgacccttacgatctgcccctagcagctatgctgatctctttgaa 1298
Db 546 TCCTTTCCCTGCTCTGCACAGTTTCGCACTGCATTAGCACGTTATGCAGATCTCTTGAA 605

QY 1299 tccctcgaagaaggcttctcgtatgctcgtcgtccgcctcatgatcgtatccca 1351
Db 606 CCCCCACGAAAAGCTGCTTTAAATTCATTAGCTGCTCATGCTTCCGAGCCTA 658

RESULT 5
AW398515 683 bp mRNA EST 18-MAY-2001
LOCUS AW398515 L. pennellii trichome, Cornell University Lycopersicon
DEFINITION EST309015
```

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pennellii cDNA clone cLPT2K2 5', mRNA sequence.
AW398515
VERSION AW398515.1 GI:6916985
KEYWORDS EST.
SOURCE Lycopersicon pennellii.
ORGANISM Lycopersicon pennellii.
REFERENCE 1 (bases 1 to 683)
AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.E.,
Liang,F., Hansen,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fujii
,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin
,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from wild tomato (Lycopersicon pennellii)
trichomes
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
Source
1..683
/organism="Lycopersicon pennellii"
/db_xref="taxon:28526"
/clone="cLPT2K2"
/tissue_type="trichome"
/dev_stage="mixed stages"
/lab_host="SOLR"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded a
mixture of cells highly enriched for trichomes, with minor
contamination by other types of leaf cells."
BASE COUNT 168 a 160 c 160 g 195 t
ORIGIN

Query Match      13.8%; Score 366.6; DB 10; Length 683;
Best Local Similarity 72.0%; Pred. No. 1.1e-79;
Matches 493; Conservative 0; Mismatches 189; Indels 3; Gaps 1;

QY 887 ctgaatacagggtagtgattcacgaacactacggtcgcggtcgtggtgataaacacataa 946
Db 2 CTGAATATCGTTTGGTTATCCATGATACCACCTAT---GAGTCTTGAGGATAAGCATGCAG 58

QY 947 atactgctaacggcgatgttgcatgttgatatctccatcctctgcagaacattgtgctc 1006
Db 59 GCATGGCTTAATGGTAATACACATATGATCCACCCCATGTCACCCCATGCAAAAGTCAATGTGGCTG 118

QY 1007 aacaaagagagctccacaaacccaaagctcgtatagatcctgtatatacatctggagttcgaca 1066
Db 119 TTCAGAGAGAGCTTACACACCCGAGTCTGATCGCTCATGCATACACTTGGAGTTTGATA 178

QY 1067 tatcaggctcttcccttacatatgagactggagatcatgttggtgtttatgctgagaact 1126
Db 179 TATCTGGCACTGGGATTTCTTATGAAACAGGAGATCATCTGGGTGTTTATGCTGAAAAATT 238

QY 1127 gcgatgaaactgcgaggaagcagggaagctgttgggtcaaccctcgtgatttgcgtgttt 1186
Db 239 CTGAGAGATACTGTTGAGGAAGCTGCGAGATTGCTGGGGCAGTCATTTAGACTTTGATATTCT 298

QY 1187 caattcacacgataaagaagacgggtccaccgccgaagagctcattaccacctcttccc 1246
Db 299 CTATTTCATACCACAAGGAGGATGTTACAGCTGGAGAGGCTCGCTACCCACCCCTTTTC 358

QY 1247 caggctcttgacccttaogatcgtccctagcacgctatgctgatcttttgaatccctcta 1306
Db 359 CTGGCCCTGCACCTCTACGTCGTGCACTTGTGTTTATGAGATCTTCTGAAATCCACCGC 418
```









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RESULT 10
BG444748
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Gossypium arboreum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 903)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGG
High quality sequence stop: 746.

FEATURES
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/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0025H01f"
/clone_lib="Gossypium arboreum 7-10 dba fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
dba"
/lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT
231 a 197 c 210 g 262 t 3 others

Query Match 13.0%; Score 343.2; DB 11; Length 903;
Best Local Similarity 67.0%; Pred. No. 6.6e-74;
Matches 508; Conservative 0; Mismatches 235; Indels 15; Gaps 1;

QY 1111 gttatgctgagaactgcgatgaaactgctcgaggaagcagggaagctgttggtcaaccc 1170
||||| ||||||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GTTACTGTGAGAACCTGGATGAAGTTGTAGATGAAGCATTCAGTTTATTGGGCTTATCA 60

QY 1171 ctggattgctgtttcaattcacacggaataaagaagcgggtcaccccgaggagctca 1230
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CCAGACACTTATTCTCTATTACACAGATTAAGAGGATGGTACACCATTGGTGAAGT 120

QY 1231 ttaccacctccttccacaggctctgcaacttacgatctgcctagcagcgtatgctgat 1290
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 TCTTTACCTTCTTCTTTCCCTTGTACTCTTAAGAACAGCAGCTGCGACGATGCTGAT 180

QY 1291 cttttgaactcctcctagaaggctctctctgattgctctgctcgcatactgtaccc 1350
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 CTTTGTAGCTGCCAAAAGAGCTGCTTACTTGTCTTGGCTGCTCATGCCCTCTGATCCA 240

QY 1351 agtgaagcagagattgctgtttttgtcatcacctctgggaaagaaatgattcaaaa 1410
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 ACTGAAGCCGATCGACTAAGACACCTTGCATCCCTGCTGGAAGATGAGTATGCACAA 300

QY 1411 tgggtagttggaagtcagaggagctcttttggagatcatgcccagtttccatcagcaaaa 1470
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 TGGATTGTTGCAACACAGAGAAGTCTCCTTGGTTCATGCGGAATTTTCTTCAGCCAG 360

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QY 1471 cccctcttggtgtgttttttctgctgagtagccctcgtcgttaaccgctcgatactattct 1530
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Db 361 CTTCCCTTTGGTGTCTTTCTTTCGACGCTGTGCTCCCAAGGTTGCAGGCTAGATATTATTC 420

QY 1531 atctcatcctcctcaagtgtgctccctcaagaattcatgtgacgtgtgcttagtatat 1590
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 ATCTCATCTCCACCAAGGATGGCCACCATCAGGATTCATGTAACCTTGTGCATTGGTTAT 480

QY 1591 ggtcaaaagccctaccggaagggttcaccgaggagtggttcgcacatggatgaagcatgca 1650
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 GAGAAAACGCCAACAGCTCGTATTACAAAAGGTCTTTGTTCAACTTGGATGAAGAATGCT 540

QY 1651 gttcc-----tcaggatagctgggtccctatttttttgcgaagcgtcaaac 1695
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GTGTCTCGGGGAAAACGCGATGACTGCAGCTGGGACCCCACTTTTGTGCGCAATCAAC 600

QY 1696 ttcaagtaccagctgaccctcaactcaattatcatctggtggacctggtacaggtta 1755
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 TTAAACTTCCCTTCAGATATAAAGTGCCCATCATANTGATTGGTCTGCTGCTGATTG 660

QY 1756 gctccttcagaggatttctgcaggaaaagtggccctcaagaaaatggtgctcaact 1815
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Db 661 GCTCCTTTCCAGGGGATTCCTTCAGAAAAGGCTTGCACTGAAAGAAGCTGGTGTGAGNTG 720

QY 1816 ggccagcagtgctcttttctggatgtagaatcgtaa 1853
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 721 GGTCCATCTGTATTGTTCTTTGGCTGCAGAACCCGNA 758

RESULT 11
BG450144
LOCUS
DEFINITION
5', mRNA
EST
16-MAR-2001
NF014G11D1F1088 Drought Medicago truncatula cDNA clone NF014G11D1
5', mRNA sequence.
ACCESSION
VERSION
BG450144.1 GI:13368926
KEYWORDS
EST.
SOURCE
barrel medic.
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 680)
Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula drought library
Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 680 Std Error: 0.00
Plate: 014 row: G column: 11
Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES
Location/Qualifiers
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/clone="NF014G11D1"
/clone_lib="Drought"
/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/notice="Vector: Lambda Zap: Contains a mixture of entire
plantlets harvested in a series of days-post-watering
timepoints."
BASE COUNT
182 a 140 c 156 g 202 t
ORIGIN

```





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/clone="GENOME SYSTEMS CLONE ID: Gm-cl049-3242"
/clone_lib="Gm-cl049"
/tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="3 week old"
/lab_host="DH10B"
/notes="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The Clark NIL was constructed and seed was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Spect, 1995). The cDNA library was constructed from mRNA
isolated from whole seedlings of 3 week old greenhouse
grown plants. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site and a 3' anchor. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoBRL). The library was constructed
in cooperation with Dr. Paul Keim's laboratory at Northern
Arizona University."
BASE COUNT      116 a      128 c      120 g      164 t
ORIGIN

Query Match      12.3%; Score 325.6; DB 11; Length 528;
Best Local Similarity 76.3%; Pred. No. 1.4e-69;
Matches 400.; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Qy 1132 gaactgtcaggaagcaggaagctgttggttcaacccctggattgctgtttcaatt 1191
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 GAACACTGTTGAAGAAACATGGGAAGTGTGGGTGAGATTTAGATCTATTTGTTCTCTT 61

Qy 1192 cacacggataaagaagcgggtccaccaggaagctctaccacctcttccccaagt 1251
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Db 62 CACACTGATAAGGAGGATGGCATTTCCCTAGTGTCTCTCTCTCTCTCTCTCTCTCT 121

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Db 122 CTTTGCACACTCGCTACTGTCATTTAGCAGCGTATGCTGATCTCTTGACCCGCCAGAAAG 181

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LOCUS
DEFINITION EST413013 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
clone cLEG3966, mRNA sequence.
ACCESSION BE461594
VERSION BE461594.1 GI:9505896
KEYWORDS EST.
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tomato.
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 590)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.B.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
,S.D.
Generation of ESTs from tomato fruit tissue, breaker stage
Unpublished (2000)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
1..590
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG3966"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/notes="Vector: pBluescriptSKmCvadapt; Site_1: EcoRI;
Site_2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopen accumulation on the blossom end of
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT      164 a      111 c      153 g      161 t      1 others
ORIGIN

Query Match      12.3%; Score 325; DB 10; Length 590;
Best Local Similarity 73.1%; Pred. No. 2e-69;
Matches 431.; Conservative 0; Mismatches 156; Indels 3; Gaps 1;

Qy 537 catggttagccacttatgtgtgtagccactgacaaatgctgcgagattttcaaatg 596
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Db 1 CATGCTGGCAACTTACGGGGATGGAGAGCAACTGATAATGCTGCAAGGTTTACAACTG 60

Qy 597 gttcactcaggaaacatgaaagggagagtggtcttcagcaactaaacttatgtgttttgg 656
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Qy 717 cggtaacaagtgtaaacgacattgttcaagtggggctcggtgacgatgatcaatgcat 776
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Db 181 GAGTGAAACAAGGTCACAAACGCTTTGTGCCCTTGTGGCTTGGTGATGATGATCAGTGCA 240

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Db 241 TGAAGATGATTTTCTGCTGGCCGAGAACAGCTGTGGCCAGAAATTTGGAATTAATTTCTTAG 300

Qy 837 agatgagagatgctcctcctcagtggtcacacggtatattgtctactgttctcgaatacag 896
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Qy 897 ggtagtattcacgaacacggtcgcggtcctggtatgataacacataaataactgtctaa 956
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Qy 957 cygcgatgttgcatattgatattctccatctcctgcagaaacctgttctcgaacaagaga 1016
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Qy 1017 gctccacaaacccaagtctgatagatcctgtatatcatctgaagttcgaatatcaggctc 1076  
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Qy 1077 ttcccttacatatgagactggagatcatgttggtgtttatgctgagaact 1126  
Db 538 TGGGATTTCCATATGAACACANGAGATCATGTGGTGTATTGCTGAAATTT 587

Search completed: December 27, 2001, 13:07:42  
Job time: 2352 sec







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; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5057 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: rat bNOS cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 349..4638
;
US-08-365-486A-12

Query Match          2.4%; Score 64.2; DB 2: Length 5057;
Best Local Similarity 47.0%; Pred. No. 3.9e-08;
Matches 306; Conservative 0; Mismatches 333; Indels 12; Gaps 3;

QY 1349 ccagtgaaacagagagattgcgtctttttgtcatcactctctgggaagaagaatgagattca 1408
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QY 1643 agcagtcagttctcagtagctgggtctctatttttttgcgaacgtcaaaacttcaagt 1702
Db 1643 agcagtcagttctcagtagctgggtctctatttttttgcgaacgtcaaaacttcaagt 1702
QY 1703 taccagctgacccctcaactcccaattatcatggtgggacctgtacaggttagctcctt 1762
Db 1703 taccagctgacccctcaactcccaattatcatggtgggacctgtacaggttagctcctt 1762
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Db 1880 taacaactctcggaacagagagtagctatttcggagctagttattgctcttttccactgtaag 1939
QY 1939 cccctgcaggcttaagacaaggcgcttccagagagctgtatcactgtctatttcccggaac 4294
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RESULT 5
US-08-880-342-12
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; Sequence 12, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5057 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
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US-08-880-342-12
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Query Match          2.4%; Score 64.2; DB 4: Length 5057;
Best Local Similarity 47.0%; Pred. No. 3.9e-08;
Matches 306; Conservative 0; Mismatches 333; Indels 12; Gaps 3;

QY 1349 ccagtgaaacagagagattgcgtctttttgtcatcactctctgggaagaagaatgagattca 1408
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Db 4295 CGGACAGCCCAAGAAATATGTACAGGAGCTGTCTGCAGGAACAGCTGGCTG 4345

RESULT 6

US-07-642-002-1  
; Sequence 1, Application US/07642002  
; Patent No. 5268465  
; GENERAL INFORMATION:  
; APPLICANT: Bredt, David S.  
; APPLICANT: Hwang, Paul M.  
; APPLICANT: Reed, Randall  
; APPLICANT: Snyder, Solomon H.  
; TITLE OF INVENTION: Purification and Molecular Cloning of Nitric  
; TITLE OF INVENTION: Oxide Synthase  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner, Birch, McKie & Beckett  
; STREET: One Thomas Circle, NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/642,002  
; FILING DATE: 19910118  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kegan, Sarah A.  
; REGISTRATION NUMBER: 32,141  
; REFERENCE/DOCKET NUMBER: 1107.033576  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 296-5500  
; TELEFAX: (202) 296-7830  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5108 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double

; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: N  
; ANTI-SENSE: N  
; ORIGINAL SOURCE:  
; ORGANISM: Rattus rattus  
; TISSUE TYPE: Brain  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 400...4686  
; OTHER INFORMATION:  
; US-07-642-002-1

Query Match 2.4%; Score 64.2; DB 1; Length 5108;  
Best Local Similarity 47.0%; Pred. No. 3.9e-08;  
Matches 306; Conservative 0; Mismatches 333; Indels 12; Gaps 3;  
QY 1349 ccagtggaacgagagatgtcgctttttgtcatcactctctgggaagaatgagatttcaa 1408  
Db 3749 CTAATGAGAAAGAGAGACGACGGTTCCTGCTCTCAGCAAGGGCTCCAGGAATATGAGG 3808  
QY 1409 aatgggtagtttggaaagtcagagaggtcttttggagatcatgcccaggtttccatcagaa 1468  
Db 3809 AGTGAAGTGGGGCAAGAACCCCAATGTTGGAGGTGCTGGAGGAGTTCCTCCGTCATCC 3868  
QY 1469 aaccctcttgggtgtgttcttcttgcagtagccccctcgtcttaaccgctcgtactatt 1528  
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Db 4226 CCATGTTCTGTGTTCTCGGTGTCGACAATCCAAAGATAGATCATATCTACAGAGAGAGA 4285  
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RESULT 7

US-07-908-245-1  
; Sequence 1, Application US/07908245  
; Patent No. 5498539  
; GENERAL INFORMATION:  
; APPLICANT: Harrison, David G.  
; APPLICANT: Alexander, R. Wayne  
; APPLICANT: Murphy, T.J.  
; APPLICANT: Nishida, Ken'ichi  
; TITLE OF INVENTION: Endothelial Nitric Oxide Synthase



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Query Match          2.2%; Score 59.2; DB 3; Length 4097;
Best Local Similarity 50.6%; Pred. No. 9.1e-07;
Matches 170; Conservative 0; Mismatches 163; Indels 3; Gaps 1;

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QY 1673 ctattttttgacagctcaaaacttaagttacacgctgacccctcaactcaattatca 1732
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QY 1733 tsgtgggaacctggtacaggttagctctcttcagaggatttttcgaggaagaatg---g 1789
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Db 3095 tsgtgggacctggtacaggttagctctccttcagaggatttttcgaggaagaatg 3154

QY 1790 cctcaagaaagtgtgtcctcaacttggcccagcagtgctctcttttcggtatgagaaac 1849
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Db 3155 acatgagagaaaaggctgcagcgcaccccatgacctggtgttcggtcgcctgct 3214

QY 1850 gtaatatggaacttatttatgagacgaactaaacaaacttcgtgaaacgagagtgatct 1909
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Db 3215 cccaaactgacctctctaccgcgacaggtgcaggaagcgcacagggcggtgttg 3274

QY 1910 cggagctgatttgcctttttcacgtgaaggagaa 1945
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Db 3275 gccggtctcaccgctctcctcccggaacctgaca 3310

RESULT 10
US-08-365-486A-18
; Sequence 18, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365.486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4353 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al.,
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..4305
US-08-365-486A-18

Query Match          2.1%; Score 55.4; DB 2; Length 4353;
Best Local Similarity 46.8%; Pred. No. 1.1e-05;
Matches 284; Conservative 0; Mismatches 311; Indels 12; Gaps 3;

QY 1349 ccagtgaaacagagattgcctttttgtcatcacctctgggaagaatgatttcaa 1408
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QY 1409 aatgggtagttggaagtcagaggagtccttttgagatcatgcccagtttccatcagcaa 1468
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Db 3425 AATGGAAATGGGGCAGAAACCCACCACCATCTGTGGAGTGTGGAGGAGTTCCCATCTATCC 3484

QY 1469 aacccctcttgggtgttctttgtcagtgagccctcgtctaccgcctcgatactatt 1528
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Db 3485 AGATGCGCGCCACCTGCTCTGACCCAGCTGTCCCTGC---TGCAGCCCGCTACTATT 3541

QY 1529 ctatctcatctctcctaagtgttgcctcctaagaattcatgtgacgtgtgttttagtat 1588
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Db 3542 CCATCAGCTCTCCCCAGACATGTACCCTGTAGTGAAGTGGACCTCACTGTGGCCATCGTTT 3601

QY 1589 atggtcaaaagcctaccggaagg-----ttcacccagaggagtggttcgacatgatga 1642
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3602 CCTACCGCACTCGAGATGGAGAAGGACCAATTACCCACGCGTATGCTCCTCTGGCTCA 3661

QY 1643 agcatgagttctcctcaggtatagctgggtcctctatttttbtgaaacgtcaaaacttcaagt 1702
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Db 3662 ACCGGATACAGGCTGACGAAGTGGTCCCTGTTTCGTGAGAGAGCACCAGCTTCACCC 3721

QY 1703 taccagctgacccctcaactccaattatcatgtggagacctggtacaggttagctcctt 1762
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Db 3722 TGCCCCGGAACCCCAAGTCCCTGTCATCTCTGTTGGACGACCGCATTTGCCCTTT 3781

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Db 3782 TCCGAAGCTTCTGGCAACAGCGGCAATTTGATATCCACACAAGGAATGAACCCCTGCC 3841

QY 1820 cagcagtgctcttttccgagatgtaggaatcgtaataatggaacttcattatgaagcagaac 1879
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Db 3842 CCATGGTCTCTGTTCTTCGGGTGCCGCAATCCAAGATAGATCATATCTACAGGGAAGAGA 3901

QY 1880 taaacaacttcgtgaaacgagagtcatttcggagctagttattgcttttcacgtgaag 1939
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3902 CCTGTGAGGCCAAGAACAAAGGGGGTCTTCAGAGAGCTGTACAGGGCTTACTCCCGGAGC 3961

QY 1940 gggaaaa 1946
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Db 3962 CAGACAA 3968

RESULT 11
US-08-880-342-18
; Sequence 18, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
```

```
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880.342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION NUMBER: US 08/365.486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4353 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human NOS-1 gene, Fujisawa, et al,
INDIVIDUAL ISOLATE: J. Neurochem 63:140 1994
FEATURE:
NAME/KEY: CDS
LOCATION: 1..4305
US-08-880-342-18

Query Match 2.1%; Score 55.4; DB 4; Length 4353;
Best Local Similarity 46.8%; Pred. No. 1.1e-05;
Matches 284; Conservative 0; Mismatches 311; Indels 12; Gaps 3;

QY 1349 ccagtgaagcagagagattgcgctttttgtcatcacctctgggaaagaatgagattcaaa 1408
DB 3365 CCAGCGAAGGAGGAGGAGCGCTGCTGCTCCTCAGCAGAGGTTTGCAGGAGTAGCAGG 3424
QY 1409 aatgggtagttggaagtcagagagagtccttttggagatcatatggccgagtttccatcagcaa 1468
DB 3425 AATGGAATGGGGCAAGAACCCACCACCATCGTGGAGGTGCTGGAGGAGTTCCTCATATCC 3484
QY 1469 aacccctcttggtgtgttcttctgtgagtagcgcctcgtctaccgcctcgatactatt 1528
DB 3485 AGATGCCGCCACCCCTGCTCTCCAGCCAGCTGCTCCCTGCG---TGCAGCCCCCGCTACTATT 3541
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DB 3542 CCATCAGCTCTCCCGCAGACATGTACCTGTAGTGAAGTGGCACCTCACTGTGGCCATCGTTT 3601
QY 1589 atggtcaagccctaccggaagg-----ttcacaggagagtggtttcgacatgagatga 1642
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QY 1643 agcatgcagttctcagagtagctgggtctctatttttttgcgaagctcaaaacttcaagt 1702
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QY 1703 taccagctgaccctccaaactccaattatcatcgtgtgggaacctgtacagaggttagctcctt 1762
DB 3722 TGCCCGGAACCCCAAGTCCCTCGTCATCTCTGTTGACCGACCGCATTTGCCCTTT 3781
QY 1763 tcagaggttttctgcaggaag---aatgcccctcaaggaataatggtcctaacttggcc 1819
DB 3782 TCCGAAGCTTCTGGCAACAGCGGCAATTGTATATCCAAACACAAGGAATGAACCCCTGCC 3841
QY 1820 cagcagtgctcttttttcggatgtaggaatcgtaatatggacttcatttatgaagacgaac 1879
DB 3842 CCATGCTCCTGCTCTTCGCGGTCCCGGCAATCCAAGATAGATCATATCTACAGGGAAGAGA 3901
QY 1880 taacaacattcgtgaacagagagtcatttcggagcagtagttatttgccttttccacgtgaag 1939
DB 3902 CCTCGAGGCCAAGAACAAAGGGGGTCTTCAGAGAGGTGTACACGGCTTACTCCCGGAGC 3961
QY 1940 gggaaaa 1946
DB 3962 CAGACAA 3968

RESULT 12
US-08-365-486A-20
; Sequence 20, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4780 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human NOS-SN gene, Nakane, et al,
; INDIVIDUAL ISOLATE: FEBS Lett 316:175 (1993)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 431..4732
; US-08-363-486A-20

Query Match 2.1%; Score 55.4; DB 2; Length 4780;
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Best Local Similarity 46.8%; Pred. No. 1.2e-05;		Query Match 2.1%; Score 55.4; DB 3; Length 4780;	
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Db	3792 CCAGCGAGAGAGAGACGACGCTCTGCTGGTCTTCAGCAAGGGTTTTCAGAGGATACGA;G 3851	Db	3792 ccagcgagaagagagacgctgctgtctctcagcaagggttttcagagtagcagg 3851
QY	1409 aatgggtagttgaaagtcagagagagtcctttttgagatcatgcccaggtttccatcagcaa 1468	QY	1409 aatgggtagttgaaagtcagagagagtcctttttgagatcatgcccaggtttccatcagcaa 1468
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QY	1469 aacccctcttgggtgttctttgtgcagtagccctcgtttaccgcctcgatactatt 1528	QY	1469 aacccctcttgggtgttctttgtgcagtagccctcgtttaccgcctcgatactatt 1528
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QY	1820 cagcagtgctcttttcggatgtagaatcgttaatatggaacttcattatgaagacgaac 1879	QY	1820 cagcagtgctcttttcggatgtagaatcgttaatatggaacttcattatgaagacgaac 1879
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Db	4329 CCTCAGGCCCAAGAACAGGGGGTCTTCAGAGAGCTGTACACGGCTTACTCCCGGAGC 4388	Db	4329 cctcgcagcgcaagaacaagggggtcttcagagagctgtacacggcttactcccgggagc 4388
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RESULT 14

US-09-123-624-3

; Sequence 3, Application US/09123624

; Patent No. 6149936

; GENERAL INFORMATION:

; APPLICANT: SCHRADER, Jurgen

; APPLICANT: GOEDECKE, Axel

; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS

; FILE REFERENCE: 511169-2003

; CURRENT APPLICATION NUMBER: US/09/123,708

; CURRENT FILING DATE: 1998-07-28

; EARLIER APPLICATION NUMBER: 08/553,503

; EARLIER FILING DATE: 1996-03-01

; EARLIER APPLICATION NUMBER: P4411402.8

; EARLIER FILING DATE: 1994-03-31

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 4780

; TYPE: DNA

; ORGANISM: Cytomegalovirus

US-09-123-708-3

US-09-123-624-3

; Sequence 3, Application US/09123624

; Patent No. 6149936

; GENERAL INFORMATION:

; APPLICANT: SCHRADER, Jurgen

; APPLICANT: GOEDECKE, Axel

; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS

; FILE REFERENCE: 511169-2004

; CURRENT APPLICATION NUMBER: US/09/123,624

; CURRENT FILING DATE: 1998-07-28

; PRIOR APPLICATION NUMBER: 08/553,503

; PRIOR FILING DATE: 1996-03-01

; PRIOR APPLICATION NUMBER: 4411402.8

; PRIOR FILING DATE: 1994-03-31

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 4780

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-123-624-3



Query Match	2.1%	Score 55.4	DB 3	Length 4780
Best Local Similarity	46.8%	Pred. No. 1.2e-05		
Matches 284	Conservative 0	Mismatches 311	Indels 12	Gaps 3

  

QY	1349	ccagtgagcagagagattgcgctcttttgc	catcacctctgggaaagaaatgagtattcaa	1408
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QY	1409	aatgggttagttggaagtcagagagtgatt	ttttggagatcatcgccgcaggtttccatcag	1468
DB	3852	aattgaaatggggcaagaaccaccatcg	tggaggctggaggaggtcccatctatcc	3911
QY	1469	aaccctcttggtgtgttctttgtctcag	tagcctctgctttaccgcctcgatactatt	1528
DB	3912	agatgcgcgcacccctgctctgaccagc	gtgccctgc--tgagccccgcgtactatt	3968
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DB	3969	ccatcagctctctcccgagacatgtacc	ctctgatgaagtcacctcactgtggccatcg	4028
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QY	1820	cagcagtgctcttttttcggatgtagga	atcgtaatatggacttcatttatgaaagac	1879
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QY	1880	tanaaactctgtggaacgaggagctat	ctatttcggagctagttatgctcttttc	1939
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QY	1940	gggaaaa	1946	
DB	4389	cagaaaa	4395	

  

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RESULT 15
US-08-880-342-20
; Sequence 20, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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# OM nucleic - nucleic search, using sw model

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12927.553 Million cell updates/sec

Title: US-09-486-757-10  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

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Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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1: em\_estfun: \*  
2: em\_esthum: \*  
3: em\_estin: \*  
4: em\_estom: \*  
5: em\_estpl: \*  
6: em\_estba: \*  
7: em\_estro: \*  
8: em\_estov: \*  
9: em\_htc: \*  
10: gb\_est1: \*  
11: gb\_est2: \*  
12: gb\_htc: \*  
13: gb\_gss: \*  
14: em\_gss\_fun: \*  
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19: em\_gss\_rod: \*  
20: em\_gss\_vrt: \*  
21: em\_gss\_other: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	29	1.1	675	10	AL505302
3	27	1.0	531	10	AW932267
4	26	1.0	415	10	AV539473
5	26	1.0	498	10	AV548760
6	26	1.0	536	10	AV546032
7	26	1.0	543	10	AI998902
8	26	1.0	601	10	AV540686
9	26	1.0	624	13	AQ958450
10	26	1.0	746	13	AQ958449
11	24	0.9	146	10	AW255611
12	23	0.9	124	10	AI705252

c 13	23	0.9	215	11	BI283532
c 14	23	0.9	245	10	AI961647
c 15	23	0.9	245	11	BE984614
c 16	23	0.9	268	10	AA669107
c 17	23	0.9	307	10	BE248453
c 18	23	0.9	312	10	AI689639
c 19	23	0.9	375	10	AI843164
c 20	23	0.9	382	11	BE988116
c 21	23	0.9	392	10	AI469773
c 22	23	0.9	402	11	BE557935
c 23	23	0.9	419	11	BE371805
c 24	23	0.9	421	11	BI276373
c 25	23	0.9	427	10	AA493217
c 26	23	0.9	438	11	BE881606
c 27	23	0.9	439	10	AW396232
c 28	23	0.9	441	11	H071233
c 29	23	0.9	456	10	BE203172
c 30	23	0.9	477	10	AL365946
c 31	23	0.9	479	10	AA924768
c 32	23	0.9	485	10	AI850041
c 33	23	0.9	496	10	AW509065
c 34	23	0.9	500	10	AW745723
c 35	23	0.9	509	10	BE057747
c 36	23	0.9	510	10	BE346181
c 37	23	0.9	512	10	AW690487
c 38	23	0.9	517	10	BE608297
c 39	23	0.9	518	11	BF003751
c 40	23	0.9	521	11	BF631848
c 41	23	0.9	526	11	BI425956
c 42	23	0.9	532	10	AW691469
c 43	23	0.9	537	10	BE347704
c 44	23	0.9	538	11	BE241454
c 45	23	0.9	541	11	BE652476

## ALIGNMENTS

### RESULT 1

AV409610 424 bp mRNA EST 23-MAY-2000  
LOCUS AV409610 Lotus japonicus young plants (two-week old) Lotus  
DEFINITION japonicus cDNA clone MML060b02\_r 5', mRNA sequence.  
ACCESSION AV409610  
VERSION AV409610.1 GI:7722464  
KEYWORDS EST.  
SOURCE Lotus japonicus.  
ORGANISM Lotus japonicus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;  
Lotus.

REFERENCE 1 (bases 1 to 424)  
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.  
TITLE Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus  
JOURNAL DNA Res. 7 (2), 127-130 (2000)  
MEDLINE 20277479  
COMMENT Contact: Yasukazu Nakamura  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: ynakamue@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

### FEATURES

source  
1. 424  
/organism="Lotus japonicus"  
/db\_xref="taxon:34305"  
/clone="MML060b02\_r"  
/clone\_lib="Lotus japonicus young plants (two-week old)"  
/dev\_stages="young plants (two-week old)"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: XhoI; Isolate=Miyakojima MG-20"  
99 a 124 c 101 g 100 t

### BASE COUNT

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ORIGIN
Query Match      1.1%; Score 29; DB 10; Length 424;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 376 ggtaactcagactggtactgctgaagatt 404
Db 340 GGTACTCAGACTGGTACTGCTGAAGATT 368

RESULT 2
AL505302
LOCUS      AL505302      675 bp      mRNA      EST      04-JAN-2001
DEFINITION AL505302 Hordeum vulgare Barke roots Hordeum vulgare cDNA clone
ACCESSION  AL505302
VERSION     AL505302.1 GI:12031517
KEYWORDS   EST.
SOURCE     barley.
ORGANISM   Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE  1 (bases 1 to 675)
AUTHORS   Michalek W., Weschke W., Pleissner K.-P. and Graner, A.
TITLE     EST sequencing and analysis in barley
JOURNAL   EST sequencing (2000)
COMMENT   Unpublished (2000)
Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5'end.
Location/Qualifiers
1..675
/organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
/clone="HW08A19V"
/clone_lib="Hordeum vulgare Barke roots"
/tissue_type="roots"
/label_host="XL0LR"
/notes="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2:
XhoI; mRNA was made from roots of spring barley variety
'Barke', a high quality malting variety. Roots were grown
for two days on filter paper at room temperature. Cloning
sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA).
NOTE: Due to a cloning artefact caused by the kit, in most
cases the EcoRI site is NOT present, as well as the EcoRI
adapter. Average insert size is 1 kb. Sequence trimming:
Vector sequences and sequence ends were trimmed from the
5'- and 3'-end until a 50 bp window contains less than two
ambiguities. The maximum length was set to 700 bp"
BASE COUNT      178 a 158 c 164 g 174 t
ORIGIN

Query Match      1.1%; Score 29; DB 10; Length 675;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1084 acatatgactggagatcatgtttggtg 1112
Db 469 ACATATGACTGGAGATCATGTGTTGTTG 497

RESULT 3
AW932267
LOCUS      AW932267      531 bp      mRNA      EST      18-MAY-2001
DEFINITION EST358110 tomato fruit mature green, TAMU Lycopersicon esculentum
cDNA clone cLEF47H10 5', mRNA sequence.
ACCESSION  AW932267

ORIGIN
Query Match      1.0%; Score 27; DB 10; Length 531;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 763 gatgataatgcatggaagatgatttt 789
Db 224 GATGATCAATGCATTGAAGATGATTTT 250

RESULT 4
AV539473/c
LOCUS      AV539473      415 bp      mRNA      EST      07-SEP-2000
DEFINITION AV539473 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
cDNA clone RZ133e03F 3', mRNA sequence.
ACCESSION  AV539473
VERSION     AV539473.1 GI:8701230
KEYWORDS   EST.
SOURCE     thale cress.
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 415)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
20363093
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

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VERSION AW932267.1 GI:8107668
KEYWORDS EST.
SOURCE   tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 531)
Alcala, J., Vrebalov, J., White, R., Mattern, A.L., Holt, I.E., Liang, F.,
Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Renning, C.M.,
Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
1..531
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEF47H10"
/clone_lib="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
/notes="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLEF - Fruit were tagged at the lcm stage and
harvested 3-5 days prior to ripening. Fruit were cut in
half to verify the seeds were indeed 'immature' and the
seeds and locules were discarded prior to freezing the
pericarp"
BASE COUNT      142 a 92 c 140 g 157 t
ORIGIN

Query Match      1.0%; Score 27; DB 10; Length 531;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 763 gatgataatgcatggaagatgatttt 789
Db 224 GATGATCAATGCATTGAAGATGATTTT 250

RESULT 4
AV539473/c
LOCUS      AV539473      415 bp      mRNA      EST      07-SEP-2000
DEFINITION AV539473 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
cDNA clone RZ133e03F 3', mRNA sequence.
ACCESSION  AV539473
VERSION     AV539473.1 GI:8701230
KEYWORDS   EST.
SOURCE     thale cress.
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 415)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
20363093
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

```

Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

# FEATURES

Location/Qualifiers  
1. 415  
/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone\_lib="Arabidopsis thaliana roots Columbia"  
/tissue\_type="roots"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 132 a 93 c 67 g 123 t  
ORIGIN

Query Match 1.0%; Score 26; DB 10; Length 415;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcacataagatgatggagaa 1979  
|||||  
Db 412 TATGTTCAACATAAGATGATGGAGAA 387

## RESULT 5

AV548760/c 498 bp mRNA EST 06-SEP-2000  
LOCUS  
DEFINITION AV548760 Arabidopsis thaliana roots Columbia Arabidopsis thaliana  
cDNA clone RZL61C08F 3', mRNA sequence.

ACCESSION AV548760  
VERSION AV548760.1 GI:8720173  
KEYWORDS EST.

SOURCE  
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 498)

AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

JOURNAL DNA Res. 7, 175-180 (2000)  
MEDLINE 20363093

COMMENT Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

# FEATURES

Location/Qualifiers  
1. 498  
/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone\_lib="Arabidopsis thaliana roots Columbia"  
/tissue\_type="roots"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 155 a 112 c 82 g 149 t  
ORIGIN

Query Match 1.0%; Score 26; DB 10; Length 498;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcacataagatgatggagaa 1979  
|||||  
Db 423 TATGTTCAACATAAGATGATGGAGAA 398

## RESULT 6

AV546032/c

LOCUS  
DEFINITION AV546032 Arabidopsis thaliana roots Columbia Arabidopsis thaliana  
cDNA clone RZL07e01F 3', mRNA sequence.

ACCESSION AV546032  
VERSION AV546032.1 GI:87117446  
KEYWORDS EST.

SOURCE  
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 536)

AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

JOURNAL DNA Res. 7, 175-180 (2000)  
MEDLINE 20363093

COMMENT Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

# FEATURES

Location/Qualifiers  
1. 536  
/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone\_lib="Arabidopsis thaliana roots Columbia"  
/tissue\_type="roots"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 170 a 122 c 90 g 154 t  
ORIGIN

Query Match 1.0%; Score 26; DB 10; Length 536;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcacataagatgatggagaa 1979  
|||||  
Db 388 TATGTTCAACATAAGATGATGGAGAA 363

## RESULT 7

AV596902/c 543 bp mRNA EST 08-SEP-1999  
LOCUS  
DEFINITION AV596902 A. thaliana, Columbia Col-0, root-2 Arabidopsis thaliana  
cDNA clone 701516529, mRNA sequence.

ACCESSION AV596902  
VERSION AV596902.1 GI:5843807  
KEYWORDS EST.

SOURCE  
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 543)

AUTHORS Chen, J., Hillebrand, J., Guebler, K., Kim, C., Doyle, M., Brzoska, P., Wang, X., Mollman, J., Griffon, J., Mouanoutoua, M., Nguyen, D., Tan, R. Gorgone, G., Burns, D., Griffon, J., Borillo, C., Carpio, T., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Pollock, J., Suzuki, G., Argentine, C., Shah, S., Nobrega, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and Hanson, D.  
TITLE Arabidopsis thaliana Gene Expression MicroArray  
JOURNAL Unpublished (1999)

COMMENT Contact: David Smoller, Ph.D.  
Genome Systems, Inc., a wholly owned subsidiary of Incyte  
Pharmaceuticals, Inc.  
4633 World Parkway Circle, St. Louis, MO 63134, USA

Tel: 877-577-2733  
 Fax: 314-427-3324  
 Email: service@genomesystems.com.

# FEATURES

source  
 1. .543  
 /organism="Arabidopsis thaliana"  
 /cultivar="Columbia Col-0"  
 /db\_xref="taxon:3702"  
 /clone="701516525"  
 /clone\_lib="A. thaliana, Columbia Col-0, root-2"  
 /tissue\_type="root"  
 /dev\_stage="4 - 7 weeks"  
 /note="vector: pSPORT; Site\_1: NotI; Site\_2: SalI; cDNA library was derived from untreated root tissue from Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks. Plants were grown in 1:1:1 peat moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C under constant light, and watered with fertilizer. cDNA synthesis was initiated using a NotI-oligo(dT) primer. Double-stranded cDNA was blunted, ligated to SalI adaptors, digested with NotI, size-selected, and cloned into the NotI and SalI sites of the pSPORT vector."  
 170 a 126 c 91 g 156 t

BASE COUNT  
 ORIGIN

Query Match 1.0%; Score 26; DB 10; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcaacataagatgatggagaa 1979

Db 380 TATGTTCAACATAGATGATGGAGAA 355

RESULT 8

AV540686/c 601 bp mRNA EST 06-SEP-2000  
 LOCUS AV540686 Arabidopsis thaliana roots Columbia Arabidopsis thaliana  
 DEFINITION cDNA clone R2153g03f 3', mRNA sequence.

ACCESSION AV540686

VERSION AV540686.1 GI:8702444

KEYWORDS EST.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 601)

AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.

TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries

JOURNAL DNA Res. 7, 175-180 (2000)

MEDLINE 20363093

COMMENT Contact: Erika Asamizu

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES

source

1. .601  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia"  
 /db\_xref="taxon:3702"  
 /clone="R2153g03f"  
 /clone\_lib="Arabidopsis thaliana roots Columbia"  
 /tissue\_type="roots"  
 /note="vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT  
 ORIGIN

184 a 137 c 97 g 183 t

Query Match 1.0%; Score 26; DB 10; Length 601;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcaacataagatgatggagaa 1979

Db 443 TATGTTCAACATAGATGATGGAGAA 418

RESULT 9

AQ958450

LOCUS LERAX59TR

DEFINITION LERAX59TR LERA Arabidopsis thaliana genomic clone LERAX59, DNA sequence.

ACCESSION AQ958450

VERSION AQ958450.1 GI:6786151

KEYWORDS GSS.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 624)

AUTHORS Buell,C.R., Lin,X., Pai,G., Barnstead,M., Bowman,C., Utterbach,T., Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.

TITLE Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms

JOURNAL Unpublished (2000)

COMMENT Contact: Xiaoying Lin

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: at@tigr.org

For additional information, see http://www.tigr.org/tdb/at/at.html

Seq primer: TR

Class: shotgun.

FEATURES

source

1. .624

/organism="Arabidopsis thaliana"

/strain="Landsberg erecta"

/db\_xref="taxon:3702"

/clone="LERAX59"

/note="Organ: Leaf; Vector: PHOS1; Total genomic DNA was sheared to 0.9-1 kbp before ligation."

BASE COUNT 175 a 114 c 134 g 199 t 2 Others

ORIGIN

Query Match 1.0%; Score 26; DB 13; Length 624;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1954 tatgttcaacataagatgatggagaa 1979

Db 488 TATGTTCAACATAGATGATGGAGAA 513

RESULT 10

AQ958449/c

LOCUS LERAX59TF

DEFINITION LERAX59TF LERA Arabidopsis thaliana genomic clone LERAX59, DNA sequence.

ACCESSION AQ958449

VERSION AQ958449.1 GI:6786150

KEYWORDS GSS.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;



```

Query Match      0.9%; Score 23; DB 10; Length 124;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2627 gagttttgagaaaaa 2649
Db 26 GAGTTTTCAGAAAAA 4

RESULT 14
LOCUS AI961647/c 245 bp mRNA EST 09-MAR-2000
DEFINITION wt65C05.x1 NCI_CGAP_Panl Homo sapiens cDNA clone IMAGE:2512328 3',
mRNA sequence.
ACCESSION AI961647
VERSION AI961647.1 GI:5754360
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1477 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 220.
Location/Qualifiers
1..245
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2512328"
/clone_lib="NCI_CGAP_Panl"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
BASE COUNT 50 a 61 c 63 g 71 t
ORIGIN

Query Match      0.9%; Score 23; DB 10; Length 245;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2627 gagttttgagaaaaa 2649
Db 33 GAGTTTTCAGAAAAA 11

RESULT 15
LOCUS BE984614/c 245 bp mRNA EST 05-OCT-2000
DEFINITION UI-M-CG0p-bdf-f-01-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
mRNA sequence.
ACCESSION BE984614
VERSION BE984614.1 GI:10657016
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery

Query Match      0.9%; Score 23; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2627 gagttttgagaaaaa 2649
Db 25 GAGTTTTCAGAAAAA 3

RESULT 13
LOCUS BI283532/c 215 bp mRNA EST 19-JUL-2001
DEFINITION UI-R-CZ0-bzc-e-10-0-UI.s1 UI-R-CZ0 Rattus norvegicus cDNA clone
mRNA sequence.
ACCESSION BI283532
VERSION BI283532.1 GI:14935371
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
TITLE Rattus.
JOURNAL 1 (bases 1 to 215)
MEDLINE Bonaldo,M.F., Lennon,G. and Soares,M.B.
COMMENT Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized penis library cDNA Library preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1..215
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CZ0-bzc-e-10-0-UI"
/clone_lib="UI-R-CZ0"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CZ0
library is a non-normalized library constructed from rat
penis tissue. For a detailed description of the library
from which this clone was derived, please visit our web
site at ratest.eng.uiowa.edu. The subtraction has been
previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
TAG_LIB=UI-R-CZ0
TAG_TISSUE=penis
TAG_SEQ=TTGCGGAACA"
BASE COUNT 43 a 55 c 54 g 63 t
ORIGIN

Query Match      0.9%; Score 23; DB 11; Length 215;
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